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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize

one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-341. The polypeptides sequences are designated SEQ ID NO: 342-682. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is unknown or any of the four bases.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-341 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-341. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-341 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-341. The sequence information can be a segment of any one of SEQ ID NO: 1-341 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-341.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information are provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-341 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-341 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-341; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-341; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-341. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-341; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in SEQ ID NO: 342-682; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a

nucleotide sequence set forth in SEQ ID NO: 1-341; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the

polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other

substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provide methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the

natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or

synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-341.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular

Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-341. The sequence information can be a segment of any one of SEQ ID NO: 1-341 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-341. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 500 amino acids, more preferably less than 200 amino acids more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by

comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells

chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include

an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2): 134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence

(*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-341; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 342-682; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 342-682. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-341; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO: 342-682; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d)

a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 342-682. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-341 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-341 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-341 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least

about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-341, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to) any one of the polynucleotides of the invention are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-341, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-341 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-341, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith,

Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-341, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et

al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-341 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-341 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced

or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE NUCLEIC ACIDS

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-341, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO: 342-682 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-341 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-341), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of an mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or

genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-341). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is

complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-341 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (In the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition,

Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the

control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No.

PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 342-682 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-341 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-341 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 342-682 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 342-682 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 342-682.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide

sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic

sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 342-682.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes,

dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference), the GeneAtlas software (Molecular Simulations Inc. (MSI), San Diego, CA) (Sanchez and Sali (1998) Proc. Natl. Acad. Sci., 95, 13597-13602; Kitson DH et al, (2000) "Remote homology detection using structural modeling – an evaluation" Submitted; Fischer and Eisenberg (1996) Protein Sci. 5, 947-955), Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark), and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a

fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs

between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals,

can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promotor of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the

polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent

stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for

generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and

cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation,

those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of

bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as

stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and

disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, vernereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of

an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In

addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation,

those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., Interpational Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present

invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of

cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without

necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-

97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide

to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis

methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol,* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol,* 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem,* 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population

expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this

invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

(ii) increased sprouting of neurons in culture or in vivo;

(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set

forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of

the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An

exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming

growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the

present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated

from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or

other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene

glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable

polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with

inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, trithanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not

increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole

weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by

periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic

indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be

prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as the amino acid sequences shown in SEQ ID NO: 342-682, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for

targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

4.13.1 POLYCLONAL ANTIBODIES

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents.

Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

4.13.2 MONOCLONAL ANTIBODIES

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly

myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

4.13.3 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the

imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

4.13.4 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature

Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in

culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

4.13.5 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

4.13.6 BISPECIFIC ANTIBODIES

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the

correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB

derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG ($Fc\gamma R$), such as $Fc\gamma RI$ (CD64), $Fc\gamma RII$ (CD32) and $Fc\gamma RIII$ (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific

antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

4.13.7 HETEROCONJUGATE ANTIBODIES

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

4.13.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

4.13.9 IMMUNOCONJUGATES

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-dilsocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-341 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-341 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE

(Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids,

more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the

polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the

invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide

encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-341, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be

selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present

invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-341. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-341 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The

technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with

secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/µl) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-Melm$_7$), is then added to a final concentration of 10 mM 1-Melm$_7$. The single-stranded DNA solution is then dispensed into CovaLink NH strips (75 µl/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-Melm$_7$, is made fresh and 25 µl added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphonate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A

lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 μg instead of 2-5 μg); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density

of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5. EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences

5.2 EXAMPLE 2

Assemblages of Novel Nucleic Acids

The nucleic acids of the present invention, designated as SEQ ID NO: 1-341 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST, gb pri, UniGene, and exons from public domain genomic sequences predicated by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), full-length gene sequences and their corresponding protein sequences were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTXY algorithm against Genbank (i.e., dbEST, gb pri, UniGene, and Genpept). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and go-zip-2 (Hyseq,

Inc.). The full-length nucleotide sequences are shown in the Sequence Listing as SEQ ID NO: 1-341. The corresponding polypeptide sequences are SEQ ID NO: 342-682.

Table 1 shows the various tissue sources of SEQ ID NO: 1-341.

The nearest neighbor results for polypeptides encoded by SEQ ID NO: 1-341 (i.e. SEQ ID NO: 342-682) were obtained by a BLASTP (version 2.0a! 19MP-WashU) search against Genpept, Geneseq and SwissProt databases using BLAST algorithm. The nearest neighbor result showed the closest homologue with functional annotation for SEQ ID NO: 1-341. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1-341 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), polypeptides encoded by SEQ ID NO: 1-341 (i.e. SEQ ID NO: 342-682) were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the Pfam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) polypeptides encoded by SEQ ID NO: 1-341 (i.e. SEQ ID NO: 342-682) were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The GeneAtlas™ software package (Molecular Simulations Inc. (MSI), San Diego, CA) was used to predict the three-dimensional structure models for the polypeptides encoded by SEQ ID NO: 1-341 (i.e. SEQ ID NO: 342-682). Models were generated by (1) PSI-BLAST which is a multiple alignment sequence profile-based searching developed by Altschul et al. (Nucl. Acids. Res. 25, 3389-3408 (1997)), (2) High Throughput Modeling (HTM) (Molecular Simulations Inc. (MSI) San Diego, CA,) which is an automated sequence and structure searching procedure (http://www.msi.com/), and (3) SeqFold™ which is a fold recognition method described by Fischer and Eisenberg (J. Mol. Biol. 209, 779-791 (1998)). This analysis was carried out, in part, by comparing the polypeptides of the invention with the known NMR (nuclear magnetic resonance) and x-ray crystal three-dimensional structures as templates. Table 5 shows, "PDB ID", the Protein DataBase (PDB) identifier given to template structure; "Chain ID", identifier of the subcomponent of the PDB template structure;

"Compound Information", information of the PDB template structure and/or its subcomponents; "PDB Function Annotation" gives function of the PDB template as annotated by the PDB files (http://www.rcsb.org/PDB/); start and end amino acid position of the protein sequence aligned; PSI-BLAST score, the verify score, the SeqFold score, and the Potential(s) of Mean Force (PMF). The verify score is produced by GeneAtlas™ software (MSI), is based on Dr. Eisenberg's Profile-3D threading program developed in Dr. David Eisenberg's laboratory (US patent no. 5,436,850 and Luthy, Bowie, and Eisenberg, Nature, 356:83-85 (1992)) and a publication by R. Sanchez and A. Sali, Proc. Natl. Acad. Sci. USA, 95:13597-12502. The verify score produced by GeneAtlas normalizes the verify score for proteins with different lengths so that a unified cutoff can be used to select good models as follows:

Verify score (normalized) = (raw score – 1/2 high score)/(1/2 high score)

The PFM score, produced by GeneAtlas™ software (MSI), is a composite scoring function that depends in part on the compactness of the model, sequence identity in the alignment used to build the model, pairwise and surface mean force potentials (MFP). As given in Table 5, a verify score between 0 to 1.0, with 1 being the best, represents a good model. Similarly, a PMF score between 0 to 1.0, with 1 being the best, represents a good model. A SeqFold™ score of more than 50 is considered significant. A good model may also be determined by one of skill in the art based all the information in Table 5 taken in totality.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determined from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al, as reference, were obtained for the polypeptide sequences. Table 6 shows the position of the last amino acid of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 7 correlates each of SEQ ID NO: 1-341 to a specific chromosomal location.

Table 8 is a correlation table of the novel polynucleotide sequences SEQ ID NO: 1-341, and their corresponding priority nucleotide sequences in the priority application USSN 09/714,936, herein incorporated by reference in its entirety.

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NO:
adult brain	GIBCO	AB3001	2 13 26-27 70 75 85 97 99-100 123 154-155 187-189
adult brain	GIBCO	ABD003	4 11 21 26-28 32 41 45 50 57 60-62 69-71 79 85 93 97 101 103-104 113 115 117 126 131 142 150 154-155 177-178 181 184 190-201 225-226 234 237 243 255-256
adult brain	Clontech	ABR001	6-7 11 14 26-27 75 93 107 131 154 201-202 243
adult brain	Clontech	ABR006	9 12 15 26-27 37 45 49 62 69 71 75 87 91 108-109 116 136 154 194 202 209 218-219 225 241 253 259 269-270 332 339
adult brain	Clontech	ABR008	2 6-7 9 12 15 18-22 26-28 35 37 40-41 45 48 50 55-56 61 63 65 67 71-76 78 85 91 94 99-101 105 108-109 117 121-123 130 140-142 145-147 149-152 154 158-159 170-174 185-186 189 198-199 201-202 205-206 212-213 220 225 228-229 236-237 240-242 248 252 255 259-262 269 272 281-282 286-287 297 302 318 326-327 339
adult brain	Clontech	ABR011	144 287
adult brain	BioChain	ABR012	23 232
adult brain	BioChain	ABR013	162
adult brain	Invitrogen	ABR014	37 40 87 253
adult brain	Invitrogen	ABR015	14 25 61 148
adult brain	Invitrogen	ABR016	40 61 124 126 225
adult brain	Invitrogen	ABT004	5 11 14-15 20 62 65 87 93-94 100 121 147 165 167 170 184-185 196 202 210 213 227 239-240 270 320
cultured preadipocytes	Stratagene	ADP001	9 14 32 61 83 108-109 118 130 173 175-176 203 225
adrenal gland	Clontech	ADR002	11 13-14 18 21 33 43 64-65 99 101-102 104-106 108-109 111 126 156 168 178 195 199 204 206 211 234 258 287
adult heart	GIBCO	AHR001	2 4 12 14-17 22 25 32-33 37 40-41 45 47-48 50 61 63-64 73-74 78 83 85 93 99 101 108-109 118 120 123-127 131 142 147 151-154 170 174 203 212 225 227-228 236 244 249 259-260 271 287
adult kidney	GIBCO	AKD001	2 4-7 9 11-12 14-15 20-25 34 40-41 47-50 53 56 60-62 65 69-72 74 76-79 82 85 87 90 93 95 97 99-100 103 108-110 113 116 118 121 123 126-129 131 140 142 145-146 155-156 162 167 193 223 225 250-251 255 287
adult kidney	Invitrogen	AKT002	4-7 9 11 14 18 21 24-25 40 42-43 53 62 73 77 79 95 110 131 151-152 158 168 185 204 211 219 222 224 245 250-251 312
adult lung	GIBCO	ALG001	5 17 25-27 34 41 65 78 85 91 97 99 104 126 135 154 175 182 211 225 233 330-331
lymph node	Clontech	ALN001	4 21 25-27 66 69 107 114 139 145-146 155 157 205 225 229
young liver	GIBCO	ALV001	4 10 12 14 24 40 59 64 94 100 103 105 121 139 154 198 234
adult liver	Invitrogen	ALV002	8 10 12 21 23 43 60 62-63 71 88 103 118 125 127 145-147 168 180 198 224 257 266 305 322-323
adult liver	Clontech	ALV003	266 337
adult ovary	Invitrogen	AOV001	2 4-7 9 11 13-16 18 21-23 25-27 33 35 37 40-41 43 45 47 52 57 60-65 67 70-71 73 78-79 82 85 87-88 90-93 95 97-99 102 104-105 111 113-114 116-118 123 126-129 131 135 142 144-147 149-153 155 159-160 164 166-172 174-175 177-179 182 185-186 190-194 196-197 206-209 219 222 225 234-237 245-248 250-254 269-270 287 296 330-331
adult placenta	Invitrogen	APL001	20 37 61 69 216
placenta	Invitrogen	APL002	32 37 46 57 62 90 149 209
adult spleen	GIBCO	ASP001	4 14 20 23 32 41 45 49 61 68 70 78 93 97 99-100 103 118 131 138 142 148 151-152 158 162 175 177 201 216 222 225 234 309
adult testis	GIBCO	ATS001	2 11 14-15 20 35 40 61 76 81 97 113 127 145-146 159 200-201 206 225 230 287
adult bladder	Invitrogen	BLD001	20 46 48 61-62 110 150 207 227 298
bone marrow	Clontech	BMD001	4 9 12 15 20 22 25-27 29 33 40-41 50-66 69-70 72 78 80-85 88 92 97 102 108-109 113 115-116 120-121 130 132 141 148 162 178 191-192

Tissue Origin	RNA Source	Library Name	SEQ ID NO:
			220 222 225 287 302
bone marrow	GF	BMD002	2 4 9 12 14-15 20-23 25-27 34-35 41-43 45 48 55-56 61-62 66 71 95 105-106 108-109 112 115-116 118 120 127 131 134 136 140-141 145-146 149 153 157 160 162 171-173 186 197 204 218 225 227 232 237 259-260 267 277 284 291 300 304 309 319 321 332 335 338
bone marrow	Clontech	BMD004	51
adult colon	Invitrogen	CLN001	13 21 87 93 97 130 140 149-150 164 199 232 250-251 266
mixture of 16 tissues/mRNAs	various vendors	CTL021	16 61 213 225
mixture of 16 tissues/mRNAs	various vendors	CTL028	61 216
adult cervix	BioChain	CVX001	2 5 14 17-18 21 32-33 40 42-43 50 61-62 64-65 70 74 78-79 82 89 92 95 97 110 114 123-124 127 155 158 168 170-172 175-177 185 197 224 234 250-251 265 287-289 333
endothelial cells	Stratagene	EDT001	2 4 11-16 18 20-21 23 26-27 32 34-35 40 42-44 47 49-50 56-57 61-63 65 70 72-74 85 88-91 93 95 99-100 106 108-110 117-118 123-124 126-129 142-143 145-146 160 175-178 190 194 204 206 209 216 225 236 262 287
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	209
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	209
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	209
fetal brain	Clontech	FBR001	21 213
fetal brain	Clontech	FBR004	299
fetal brain	Clontech	FBR006	4 6-7 9 12 15 18-19 21 28-29 35 37 40 50 62 67 76 78 91 99 108-109 112 117 141 149 151-152 154 157 159 177 185 196 201-202 204 212 218 225 241 255 259 271 281 287 290 299-300 313 332 339
fetal brain	Invitrogen	FBT002	11-12 14 56 62 74 91 96 127 149 160 178-179 184-185 193 206 214 225 237 241-243
fetal heart	Invitrogen	FHR001	5 14 21 28 35 64-66 78 101 106 113 149 151-152 158 160 162 186 204 218 229 248 311 330-331 339-340
fetal kidney	Clontech	FKD001	12 23 33 40 61 69 82 91 98 104 155 175
fetal kidney	Clontech	FKD002	151-152 204 206 218 224 248 287
fetal kidney	Invitrogen	FKD007	25 61
fetal lung	Clontech	FLG001	21 35 126 159 203
fetal lung	Invitrogen	FLG003	6-7 14 23 45 48 56 61 121 149 154 164 180 234 248 250-251 330-331
fetal liver-spleen	Columbia University	FLS001	1-14 16-25 28-49 55 57 59 61-65 74 77-78 80 87-91 93-108 110-112 114 117-118 120-121 128-129 131 136 142-143 149 151-153 155 162 180-182 186 193 196 207 210-211 213 217-219 222 224 248 284 287 294 304 316 322

Tissue Origin	RNA Source	Library Name	SEQ ID NO:
fetal liver-spleen	Columbia University	FLS002	3-5 8 10 12-13 17 20-21 23-27 30-33 35-37 39-40 44 57 59 63-65 71-72 74 77 79 88-89 93-95 97 99 101 103-107 111 114-115 117-118 121-122 127-129 131 142 149 158 160 173 175-176 178 181-182 185 191-193 196 206-207 209-210 216-220 229 236 243 245-246 248-249 257 277 294-296 311 317-318 325 341
fetal liver-spleen	Columbia University	FLS003	14 20 126 160 249 294 319 334
fetal liver	Invitrogen	FLV001	6-7 10 12 14 16 24 33 37 48 50 143 149 151-152 158 186 196 224 238
fetal liver	Clontech	FLV002	14 21 61 149 335
fetal liver	Clontech	FLV004	10 14 21 24 29 34-35 37 45 47 69 72 108-109 116 118 139 157 179 255 332
fetal muscle	Invitrogen	FMS001	21 26-27 32 35 37 44 61 94 108-109 118 124 126-127 134 159 190 216 263
fetal muscle	Invitrogen	FMS002	14 21-22 42-43 67-68 85 108-109 117 118-119 145-146 185 198 216 262-263 332 336 339
fetal skin	Invitrogen	FSK001	2 10-14 17 28 33 37 40 46 59 62-63 68-69 71 81 90 93 100 115 122 127 131 143 150 153 156 160 174 195-196 206 213 216 224-225 239 287 301-302 313-315
fetal skin	Invitrogen	FSK002	2 22 34 41 66 71 100 113-114 116 121 143 178-179 194 209 216 227 259 267 313
fetal spleen	BioChain	FSP001	21 91
umbilical cord	BioChain	FUC001	2 14 17 21 25-27 33 42-43 45 48 60-62 78 85-86 90 93 97 99 103 107 110 116-117 126 147 151-152 161 168 216 220 234 236 285
fetal brain	GIBCO	HFB001	14-15 18 21 23 26-28 32 35 40-41 43 47 60 67-68 70-79 85 94 99 101 144-146 149 151-152 158 177 183-184 197 212-213 225
infant brain	Columbia University	IB2002	4-5 9 11-12 14 16 21 28-29 35 37 47-48 64 68 71-72 75 79 91-93 99-100 103 106 121 126 131 147 151-152 154-155 159 162 177 182 185-187 201 209 211 213-214 223 246 267 271 309 319-320 328
infant brain	Columbia University	IB2003	4-5 9 21 26-28 45 79 90 92-93 131 147-148 185 191-192 205 213-214 336
infant brain	Columbia University	IBM002	21 75 320
infant brain	Columbia University	IBS001	21 150 185 320
fibroblast	Stratagene	LFB001	2 13-14 18 26-27 33 40 42-43 93 99 111 116 123 126 133 137 150 155 175-176 201 216 225 245 329
adult lung	Invitrogen	LGT002	5-7 11 14 20-21 26-27 33 35 37 40-43 47-48 53 59 61-62 72 74 79 81 83 85 90-91 95 97 99-100 104 106-107 111 117-118 126-127 136 139-140 142 145-146 153 155 160 162 164 170 175-176 181-182 203 206 215-216 220-225 233-235 248-251 262 268 291 309-310 330-331
lymphocytes	ATCC	LPC001	4 9 14 21 26-27 41 50 61 69 85 100 107 113 117-118 120 131 137 164 170-172 209 225 227 245 247 275 286 319
leukocyte	GIBCO	LUC001	1-2 4-5 9 12-15 20-22 25-27 33 35 38 40-43 50 53 57 59-63 65 69 71-72 74 76 78-79 82-83 88 93 95 97-99 101 103 107-109 113-114 116-120 123 126 131 133-139 150 161-165 173 178 218 222 225 227 250-251 273-275 287 305-307 309 319 338
leukocyte	Clontech	LUC003	4-5 12 42-43 63 71 99 116 118 148 162 166 171-172 309
melanoma fro mcell line ATCC #CRL 1424	Clontech	MEL004	2 9 12 20 26-27 70 72 79 100 113 116 126 147-148 168 184 218 225 284 304
mammary gland	Invitrogen	MMG001	5-7 12-16 20-21 28 32 45-46 48 59 61-62 65 71 74 79 90-91 93-94 97 100 102-103 110 115 118 121-122 131 139 149 162 167 169 196 198 206-207 216 220 222 224-225 233 236 245 255-258 287 311 330-331 339
induced	Stratagene	NTD001	13-14 26-27 32 61 65 72 78

Tissue Origin	RNA Source	Library Name	SEQ ID NO:
neuronal cells			
retinoic acid-induced neuronal cells	Stratagene	NTR001	14 16 44 231 249
neuronal cells	Stratagene	NTU001	5 13-14 16 21 68 72 74 115 150 160 170
pituitary gland	Clontech	PIT004	9 34 69 74 85 99 270 333
placenta	Clontech	PLA003	9 35 37 45 64 87 93 99 113 116 139 164 218
prostate	Clontech	PRT001	14 17 21-22 33-34 63-64 79 85 93 99 111 158 200 225 245 262 275
rectum	Invitrogen	REC001	5-7 13 20 41 61-63 93 100 110-111 130 149 158 199 206 218 223 245 302-303 320
salivary gland	Clontech	SAL001	5 14 23 61 70 91 105 111 137 162 245 276 285
skin fibroblast	ATCC	SFB002	225
small intestine	Clontech	SIN001	12 14 17 21-22 41 44 46-47 60 62 71-72 83 86 94 100 105 121 126 131 136 138 171-173 175 183 185 203 205 207 216-217 233 235 238-239 245 250-251 276 285 335
skeletal muscle	Clontech	SKM001	12 14 26-27 35 76 91 103 118 263
spinal cord	Clontech	SPC001	5 14 21-22 25-27 34 45 48 61 67 70-71 76 91 95 118 126-127 154 173 190 212 222 225 281
Adult spleen	Clontech	SPL001	1 33 41 121 222
stomach	Clontech	STO001	4 21 25-27 38 53 61 63 76 104 111 115 155 215 225 238 262 275 277
thalamus	Clontech	THA002	20 37 74 111 114 130 149 187 193 206 209 216 250-251 253 261
thymus	Clontech	THM001	4 9 14 18 21 23 26-27 41-43 59 61 69 83 95 100 106 114 124 126 128-129 133 155 170 178 245 258 277
thymus	Clontech	THM002	12 20-21 26-27 35 40 48 59 61-62 64 66 69 78 94 99 106-109 112-113 118 126-129 140 157 161-162 164 170 173 191-192 208-209 213 221-222 253 260 278 286 291-292 305 307-309 316
thyroid gland	Clontech	THR001	4-7 11-12 14-15 18 21-23 33 35 40 46 59 69-74 76 78 83 85-86 91 93 97 105-106 108-109 114 117 123 126 131 138-139 145-146 151-153 165 173 190 194 206 225 234 263 265 276 279-280 293 297 324
trachea	Clontech	TRC001	49-50 60 62 73-74 76 88 134 178 225 250-251 264-265
uterus	Clontech	UTR001	2 5 12 14 17 21 26-27 33 50 69 85 97 117 138

The 16 tissue/mRNAs and their vendor sources are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) Normal adult kidney mRNA (Invitrogen), 3) Normal fetal brain mRNA (Invitrogen), 4) Normal adult liver mRNA (Invitrogen), 5) Normal fetal kidney mRNA (Invitrogen), 6) Normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) Human bone marrow mRNA (Clontech), 10) Human leukemia lymphoblastic mRNA (Clontech), 11) Human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human so\spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
342	AK027819	Homo sapiens	FLJ14913 fis, clone PLACE1006782.	2806	100
343	AAB81047	Homo sapiens	20-JUN-2001 28-JUL-1999 Human protein HP00698 amino acid sequence.	1708	100
344	AB040926	Homo sapiens	for KIAA1493 protein, partial cds.	1973	98
345	AAB01382	Homo sapiens	20-OCT-2000 10-DEC-1999 Neuron-associated protein.	4363	99
346	AAY99410	Homo sapiens	08-AUG-2000 01-SEP-1999 Human PRO1480 (UNQ749) amino acid sequence SEQ ID NO:253.	3576	99
347	AAE01114	Homo sapiens	17-JUL-2001 08-NOV-2000 Human gene 1 encoded secreted protein HBINK72, SEQ ID NO:28.	2767	99
348	AAE01114	Homo sapiens	17-JUL-2001 08-NOV-2000 Human gene 1 encoded secreted protein HBINK72, SEQ ID NO:28.	1652	76
350	AF113208	Homo sapiens	mRNA, complete cds.	1615	100
351	AAB49535	Homo sapiens	09-MAR-2001 06-APR-2000 Clone HFKCD20.	3027	100
352	BC001079	Homo sapiens	clone MGC:2731 IMAGE:2822460, mRNA, complete cds.	1127	99
353	AAB20093	Homo sapiens	23-APR-2001 16-JUN-2000 Human hydrophobic domain-containing protein HP03374.	803	100
354	AY007148	Homo sapiens	CDABP0084 mRNA sequence.	984	100
355	BC001795	Homo sapiens	Similar to ribosomal protein S2, clone MGC:3141 IMAGE:3353508, mRNA, complete cds.	971	100
356	BC008739	Homo sapiens	protein x 013, clone MGC:3073 IMAGE:3346340, mRNA, complete cds.	386	100
357	AY007133	Homo sapiens	CDABP0047 mRNA sequence.	1639	95
358	X15977	Homo sapiens	mRNA for collagen VI alpha-2 alternative C-terminal domain.	515	100
359	BC013173	Homo sapiens	clone MGC:17340 IMAGE:4340287, mRNA, complete cds.	3049	100
360	BC011747	Homo sapiens	Similar to secretory carrier membrane protein 4, clone MGC:19661 IMAGE:3161979, mRNA, complete cds.	1022	87
363	AJ310550	Homo sapiens	for SMC5 protein.	3517	99
364	AJ276485	Homo sapiens	for putative integral membrane transporter protein (LC27 gene).	1502	100
365	J05158	Homo sapiens	carboxypeptidase N mRNA, 3' end.	2274	88
366	X57351	Homo sapiens	1-8D gene from interferon-inducible gene family.	673	97
367	AF230904	Homo sapiens	protein (CIN85) mRNA, complete cds.	3437	100
368	AF230904	Homo sapiens	protein (CIN85) mRNA, complete cds.	2615	99
369	AJ236915	Homo sapiens	for pak5 protein.	3550	100
370	AF269253	Homo sapiens	apyrase-like protein 1 (LALP1) mRNA, complete cds.	3198	100
373	AAY24791	Homo sapiens	26-AUG-1999 18-DEC-1998 Human secreted protein sm134 4.	1277	100
374	X68277	Homo sapiens	CL 100 mRNA for protein tyrosine phosphatase.	1886	100
375	AK025844	Homo sapiens	FLJ22191 fis, clone HRC01066.	1904	100
376	AF032668	Rattus	raec15	3738	92

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		norvegicus			
378	AF195534	Rattus norvegicus	GERp95	4513	99
379	AAG63221	Homo sapiens	01-OCT-2001 18-JAN-2001 Amino acid sequence of a human lipid metabolism enzyme.	518	100
380	AAB68878	Homo sapiens	24-APR-2001 21-JUL-2000 Human RECAP polypeptide, SEQ ID NO: 8.	946	100
381	BC004546	Homo sapiens	disrupter of silencing 10, clone MGC:11290 IMAGE:3946633, mRNA, complete cds.	2431	100
382	AAY02361	Homo sapiens	13-JUL-1999 06-OCT-1998 Polypeptide identified by the signal sequence trap method.	979	98
383	AAB63460	Homo sapiens	26-MAR-2001 26-MAY-2000 Human breast cancer associated antigen protein sequence SEQ ID NO:822.	984	99
384	AAB63460	Homo sapiens	26-MAR-2001 26-MAY-2000 Human breast cancer associated antigen protein sequence SEQ ID NO:822.	984	99
385	BC001068	Homo sapiens	clone IMAGE:2823731, mRNA, partial cds.	2994	99
386	AK003950	Mus musculus	putative	623	97
387	AK001527	Homo sapiens	FLJ10665 fis, clone NT2RP2006200.	4109	99
388	BC014442	Homo sapiens	clone MGC:22964 IMAGE:4866321, mRNA, complete cds.	2333	100
389	BC000056	Homo sapiens	clone MGC:3262 IMAGE:3506385, mRNA, complete cds.	1464	95
390	BC004393	Homo sapiens	Similar to RIKEN cDNA 2310045B01 gene, clone MGC:10974 IMAGE:3635540, mRNA, complete cds.	1145	99
391	AK026302	Homo sapiens	FLJ22649 fis, clone HSI07332.	930	99
392	AK001411	Homo sapiens	FLJ10549 fis, clone NT2RP2001976, moderately similar to Mus musculus calmodulin-binding protein SHA1 mRNA.	3711	100
393	AAB93202	Homo sapiens	26-JUN-2001 28-JUL-2000 Human protein sequence SEQ ID NO:12168.	2549	99
394	AAG75102	Homo sapiens	03-SEP-2001 28-SEP-2000 Human colon cancer antigen protein SEQ ID NO:5866.	995	100
396	AF006088	Homo sapiens	protein complex subunit p16-Arc (ARC16) mRNA, complete cds.	371	100
397	BC005131	Homo sapiens	Similar to RIKEN cDNA 2010003J03 gene, clone MGC:11102 IMAGE:3831647, mRNA, complete cds.	849	99
398	AK010289	Mus musculus	putative	854	73
399	AF226055	Homo sapiens	(HTON29) mRNA, complete cds.	1367	100
400	AF090910	Homo sapiens	HQ0478 PRO0478 mRNA, complete cds.	180	89
401	AF118084	Homo sapiens	PRO1914	350	98
402	BC007283	Homo sapiens	ribosomal protein S11, clone MGC:15628 IMAGE:3343839, mRNA, complete cds.	824	100
403	AK025392	Homo sapiens	FLJ21739 fis, clone COLF4061.	4331	99
404	AF077615	Homo sapiens	beta inducible nuclear protein TINP1 (TINP1) mRNA, complete cds.	1364	100
405	AK027709	Homo sapiens	FLJ14803 fis, clone NT2RP4001442.	2963	99
406	BC006002	Homo sapiens	Similar to RIKEN cDNA 1190005P17 gene, clone MGC:14817 IMAGE:4247279, mRNA, complete cds.	666	100
407	M80902	Homo sapiens	AHNAK nucleoprotein mRNA, 3' end.	8529	99
408	AAW90962	Homo sapiens	14-JUL-2000 06-NOV-1998 Human CSGP-2	2346	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			protein.		
409	AK027715	Homo sapiens	FLJ14809 fis, clone NT2RP4001822, weakly similar to PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3.	1295	100
410	BC015928	Homo sapiens	clone MGC:8773 IMAGE:3908916, mRNA, complete cds.	2186	100
411	BC015317	Homo sapiens	Similar to suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein), clone MGC:21083 IMAGE:4425762, mRNA, complete cds.	302	100
412	L26335	Cavia porcellus	zinc finger protein	1493	99
413	AF209198	Homo sapiens	finger protein 277 (ZNF277) mRNA, complete cds.	2357	100
414	AE001399	Plasmodium falciparum	OAF domain protein (cyclic nt signal transduct.)	178	35
415	AAY48226	Homo sapiens	08-DEC-1999 10-MAR-1998 Human prostate cancer-associated protein 12.	1204	96
416	M94389	Loligo pealei	neurofilament protein	165	23
417	AF317425	Homo sapiens	(GAC-1) mRNA, complete cds.	3725	91
418	AF116675	Homo sapiens	PRO1942	257	100
419	AAG73932	Homo sapiens	03-SEP-2001 28-SEP-2000 Human colon cancer antigen protein SEQ ID NO:4696.	1415	100
420	AK000100	Homo sapiens	FLJ20093 fis, clone COL04263.	841	100
421	BC005326	Homo sapiens	ribosomal protein L27a, clone MGC:12412 IMAGE:4052417, mRNA, complete cds.	754	99
422	AF119865	Homo sapiens	PRO2176	470	97
424	AF138863	Homo sapiens	PRO1677	868	99
425	X14361	Homo sapiens	CR1 gene for C3b/C4b receptor SCR9 (or 16) C-term. exon SCR = short consensus repeat.	135	100
426	Z24725	Homo sapiens	mitogen inducible gene mig-2, complete CDS.	3576	99
427	AK027587	Homo sapiens	FLJ14681 fis, clone NT2RP2004270, weakly similar to PROTEIN PTM1 PRECURSOR.	1103	100
428	AC004770	Homo sapiens	11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.	1527	84
429	AK026262	Homo sapiens	FLJ22609 fis, clone HSI04913.	1795	99
430	BC007279	Homo sapiens	clone FLB5214, clone MGC:15622 IMAGE:3343280, mRNA, complete cds.	416	100
431	AL133035	Homo sapiens	cDNA DKFZp434G171 (from clone DKFZp434G171).	1136	99
432	AF166125	Homo sapiens	N mRNA, partial cds.	1816	99
433	AF161370	Homo sapiens	mRNA, partial cds.	824	100
434	AK000161	Homo sapiens	FLJ20154 fis, clone COL08740.	284	100
435	AK001784	Homo sapiens	FLJ10922 fis, clone OVARC1000420.	684	100
436	BC011396	Homo sapiens	clone MGC:17720 IMAGE:3870711, mRNA, complete cds.	1080	100
437	AF165527	Homo sapiens	(DGCR8) mRNA, complete cds.	859	100
438	AF230200	Homo sapiens	mRNA, partial cds.	358	95
439	BC008468	Homo sapiens	Similar to RIKEN cDNA 1110039G10 gene, clone MGC:14734 IMAGE:4277104, mRNA, complete cds.	791	100
440	BC007870	Homo sapiens	DC6 protein, clone MGC:14435 IMAGE:4303290, mRNA, complete cds.	505	100
441	AAB20167	Homo sapiens	30-APR-2001 17-JUL-2000 Human protein	2066	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			associated with IgA nephropathy.		
442	AAB08910	Homo sapiens	30-AUG-2000 22-SEP-1999 Human secreted protein sequence encoded by gene 20 SEQ ID NO:67.	1112	100
443	BC003026	Homo sapiens	clone IMAGE:2823490, mRNA, partial cds.	354	84
444	BC003127	Homo sapiens	Similar to sclenoprotein X, 1, clone MGC:3344 IMAGE:2905838, mRNA, complete cds.	527	100
445	AK000143	Homo sapiens	FLJ20136 fis, clone COL07068.	2260	100
446	AK000388	Homo sapiens	FLJ20381 fis, clone KAIA2329.	2375	100
447	BC002364	Homo sapiens	non-POU-domain-containing, octamer-binding, clone MGC:8677 IMAGE:2964534, mRNA, complete cds.	2449	98
448	AK025645	Homo sapiens	FLJ21992 fis, clone HEP06554.	920	88
449	AAB95268	Homo sapiens	26-JUN-2001 28-JUL-2000 Human protein sequence SEQ ID NO:17462.	3708	99
450	AF113538	Homo sapiens	x receptor interacting protein mRNA, complete cds.	1800	100
451	AAW78167	Homo sapiens	13-APR-1999 11-JUN-1998 Human secreted protein encoded by gene 42 clone HFAT33.	795	100
452	BC014943	Homo sapiens	NMN adenylyltransferase; nicotinamide mononucleotide adenylyl transferase, clone MGC:22925 IMAGE:4874147, mRNA, complete cds.	1458	100
453	BC000348	Homo sapiens	ribosomal protein L35, clone MGC:8582 IMAGE:2960987, mRNA, complete cds.	593	97
454	AJ277591	Homo sapiens	for p15-2a protein (p15-2 gene).	749	100
455	AK000927	Homo sapiens	FLJ10065 fis, clone HEMBA1001455.	3143	100
456	AB045118	Homo sapiens	mRNA, complete cds.	1192	99
457	AAZ51355	Homo sapiens	06-JUN-2000 20-AUG-1999 Human wild type serine/threonine kinase KIS (hKIS) gene.	2198	99
458	AF146696	Homo sapiens	pAB195 FOXP1 (FOXP1) mRNA, complete cds.	1639	100
459	BC009401	Homo sapiens	natural killer cell transcript 4, clone MGC:15353 IMAGE:4300407, mRNA, complete cds.	914	100
460	BC010537	Homo sapiens	activated RNA polymerase II transcription cofactor 4, clone MGC:17295 IMAGE:3457167, mRNA, complete cds.	563	99
461	AF076642	Homo sapiens	of O-protein signaling 13 mRNA, complete cds.	1218	100
462	AF116718	Homo sapiens	PRO2900	396	100
463	AAB18919	Homo sapiens	08-FEB-2001 01-MAR-2000 A novel polypeptide designated PRO4356.	1137	99
464	AC025416	Arabidopsis thaliana	F5O11.12	135	36
465	BC002757	Homo sapiens	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle), clone MGC:3716 IMAGE:3631740, mRNA, complete cds.	247	100
466	AY037115	Homo sapiens	stromal lymphopoietin (TSLP) mRNA, complete cds.	823	100
467	M15841	Homo sapiens	U2 small nuclear RNA-associated B" antigen mRNA, complete cds.	638	100
468	AK026916	Homo sapiens	FLJ22263 fis, clone COL06129.	2612	99
469	AAY05317	Homo sapiens	25-JUN-1999 08-SEP-1998 Human secreted protein bn97 1.	1508	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
470	AAY05317	Homo sapiens	25-JUN-1999 08-SEP-1998 Human secreted protein bn97 1.	851	99
471	AAY66721	Homo sapiens	05-APR-2000 02-JUN-1999 Membrane-bound protein PRO511.	1176	93
472	AAB12144	Homo sapiens	02-FEB-2001 17-NOV-1999 Hydrophobic domain protein isolated from WERI-RB cells.	1806	100
474	AL022398	Homo sapiens	sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.	575	100
475	AF324830	Homo sapiens	transcript 11 protein (IL-T11) mRNA, complete cds.	1590	100
476	AJ306731	Homo sapiens	for RhoGAP protein (RICH1 gene).	846	100
477	BC006116	Homo sapiens	Similar to RIKEN cDNA 3100002B05 gene, clone MGC:12993 IMAGE:3504453, mRNA, complete cds.	2063	100
478	AK001077	Homo sapiens	FLJ10215 fis, clone HEMBA1006737, weakly similar to ANKYRIN, BRAIN VARIANT 2.	812	100
479	AAG89322	Homo sapiens	11-SEP-2001 07-DEC-2000 Human secreted protein, SEQ ID NO: 442.	922	98
480	AAE02782	Homo sapiens	06-AUG-2001 06-DEC-2000 Human six transmembrane epithelial antigen of prostate (STEAP)-3 protein.	2392	100
481	AK025537	Homo sapiens	FLJ21884 fis, clone HEP02863.	3021	99
482	AJ007590	Homo sapiens	for XRP2 protein.	1766	100
483	AAG93264	Homo sapiens	13-SEP-2001 06-DEC-2000 Human protein HP10160.	841	100
484	AB027258	Homo sapiens	for basal transcriptional activator hABT1, complete cds.	1408	100
485	BC000518	Homo sapiens	Similar to brain acid-soluble protein 1, clone MGC:8555 IMAGE:2822874, mRNA, complete cds.	1137	99
486	AK001425	Homo sapiens	FLJ10565 fis, clone NT2RP2002769.	1695	99
487	BC013322	Homo sapiens	clone MGC:13411 IMAGE:4077631, mRNA, complete cds.	1459	99
488	AK002030	Homo sapiens	FLJ11168 fis, clone PLACE1007274.	1029	100
489	BC003378	Homo sapiens	high-mobility group (nonhistone chromosomal) protein 1, clone MGC:5223 IMAGE:2901382, mRNA, complete cds.	1140	99
490	AK001159	Homo sapiens	FLJ10297 fis, clone NT2RM1001074.	764	100
491	AK000020	Homo sapiens	FLJ20013 fis, clone ADKA03455.	1613	100
492	AK001322	Homo sapiens	FLJ10460 fis, clone NT2RP1001475.	1207	100
493	AK001322	Homo sapiens	FLJ10460 fis, clone NT2RP1001475.	892	98
494	AY008293	Homo sapiens	protease (SENP8) mRNA, complete cds.	1114	99
495	AF413080	Homo sapiens	mRNA, complete cds.	9184	99
496	AK000154	Homo sapiens	FLJ20147 fis, clone COL07954.	673	100
497	AK001001	Homo sapiens	FLJ10139 fis, clone HEMBA1001175.	658	100
498	AK027124	Homo sapiens	FLJ23471 fis, clone HSI11969.	1773	99
501	BC012024	Homo sapiens	kinetochore protein CENP-H, clone MGC:21431 IMAGE:4510607, mRNA, complete cds.	1214	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
502	U40407	synthetic construct	T cell receptor alpha chain	1119	80
503	AF043179	Homo sapiens	cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds.	681	73
504	AF116678	Homo sapiens	PRO1995	587	100
505	AB051853	Homo sapiens	gene for rho-GTPase activating protein, complete cds.	1766	98
506	AB046074	Macaca fascicularis	unnamed protein product	515	83
507	AK002848	Mus musculus	putative	429	84
508	AAB08973	Homo sapiens	30-AUG-2000 22-SEP-1999 Human secreted protein sequence encoded by gene 27 SEQ ID NO:130.	1753	98
509	AK000740	Homo sapiens	FLJ20733 fis, clone HEP08550.	4651	100
510	AL136858	Homo sapiens	cDNA DKFZp434N2435 (from clone DKFZp434N2435); complete cds.	501	100
511	BC008413	Homo sapiens	clone MGC:14552 IMAGE:4333593, mRNA, complete cds.	1706	99
513	AJ277275	Homo sapiens	for rapa-1 (rapa gene).	5086	100
514	AB042563	Homo sapiens	mRNA for casein kinase 1 gamma 1L, complete cds.	1739	100
515	BC015597	Homo sapiens	clone IMAGE:4649498, mRNA, partial cds.	719	63
516	BC001277	Homo sapiens	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, clone MGC:5099 IMAGE:3462392, mRNA, complete cds.	1103	100
517	AF081126	Drosophila melanogaster	ER lumen protein retaining receptor	409	75
519	AK023651	Homo sapiens	FLJ13589 fis, clone PLACE1009308, weakly similar to GLUCOSE REPRESSION MEDIATOR PROTEIN.	1488	100
520	AK000371	Homo sapiens	FLJ20364 fis, clone HEP17854.	2040	100
522	AAB24228	Homo sapiens	07-FEB-2001 06-APR-2000 Human vesicle associated protein 7 SEQ ID NO:7.	1293	100
523	BC015387	Homo sapiens	Similar to RIKEN cDNA 1110001O19 gene, clone MGC:21689 IMAGE:4400374, mRNA, complete cds.	429	100
524	BC008488	Homo sapiens	RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds.	404	97
526	AF360739	Homo sapiens	protein S5-56 (S5-56) mRNA, complete cds.	2618	99
527	BC013723	Homo sapiens	clone MGC:17998 IMAGE:3922049, mRNA, complete cds.	782	100
529	AF230201	Homo sapiens	mRNA, complete cds.	396	100
530	AK001984	Homo sapiens	FLJ11122 fis, clone PLACE1006139.	658	100
531	AK000530	Homo sapiens	FLJ20523 fis, clone KAT10456.	691	100
532	U37134	Drosophila melanogaster	inturned protein	248	23
533	U37134	Drosophila melanogaster	inturned protein	244	23
535	AB033133	Homo sapiens	complete cds, testis-specific gene2.	1586	100
536	AF153417	Homo sapiens	9 open reading frame 6 mRNA, complete cds.	221	100
537	AJ277557	Homo sapiens	gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5.	617	100
538	AF127564	Arabidopsis	ubiquitin-protein ligase 1	854	42

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		thaliana			
540	AK000442	Homo sapiens	FLJ20435 fis, clone KAT03864.	1513	99
541	AF278541	Homo sapiens	protein ACT mRNA, complete cds.	1657	99
542	AAY99440	Homo sapiens	08-AUG-2000 01-SEP-1999 Human PRO1564 (UNQ770) amino acid sequence SEQ ID NO:347.	3408	100
543	AL117491	Homo sapiens	cDNA DKFZp434N231 (from clone DKFZp434N231); partial cds.	7295	100
544	BC003179	Homo sapiens	clone MGC:4419 IMAGE:2958058, mRNA, complete cds.	992	100
545	AAE05186	Homo sapiens	13-SEP-2001 12-JAN-2001 Human drug metabolising enzyme (DME-17) protein.	1095	99
546	AAY94926	Homo sapiens	16-JUN-2000 13-AUG-1999 Human secreted protein clone rd232_5 protein sequence SEQ ID NO:58.	1578	99
547	AK026027	Homo sapiens	FLJ22374 fis, clone HRC06766.	647	100
548	AL137584	Homo sapiens	cDNA DKFZp434O1310 (from clone DKFZp434O1310); partial cds.	246	97
550	AF352026	Homo sapiens	protein 1 mRNA, complete cds.	3085	99
552	AK025840	Homo sapiens	FLJ22187 fis, clone HRC01029.	918	100
553	BC013117	Homo sapiens	clone MGC:8711 IMAGE:3842749, mRNA, complete cds.	1126	100
554	BC014111	Homo sapiens	Similar to ecotropic viral integration site 5, clone MGC:20844 IMAGE:4542709, mRNA, complete cds.	2698	97
555	AK016622	Mus musculus	putative	1413	97
557	AF181263	Homo sapiens	domain containing 2 (EHD2) mRNA, complete cds.	2816	99
558	AP001660	Homo sapiens	DNA, chromosome 21q, section 4/105.	1424	100
559	BC001781	Homo sapiens	ribosomal protein L44, clone MGC:2064 IMAGE:3351669, mRNA, complete cds.	542	100
560	AF081941	Rattus norvegicus	soluble adenylyl cyclase	142	38
561	AF378129	Homo sapiens	domain containing adaptor protein TIRAP mRNA, complete cds.	1227	99
562	X01403	Homo sapiens	mRNA fragment for T-cell receptor alpha chain.	840	90
563	AAY39883	Homo sapiens	07-DEC-1999 26-MAR-1999 MHC Class II p41 specific region.	947	99
564	AB026707	Homo sapiens	for FOAP-11 protein, complete cds.	429	100
565	AK007905	Mus musculus	putative	1484	83
566	BC015589	Homo sapiens	clone IMAGE:4401937, mRNA, partial cds.	421	100
567	AF116669	Homo sapiens	PRO1828	237	100
568	AK000328	Homo sapiens	FLJ20321 fis, clone HEP09380.	5507	99
569	AF263913	Mus musculus	fidgetin	3864	97
570	AK015017	Mus musculus	putative	635	50
572	AK001673	Homo sapiens	FLJ10811 fis, clone NT2RP4000955.	3661	100
573	AAY96059	Homo sapiens	05-DEC-2000 02-MAR-2000 Human sphingosine kinase C.	617	100
574	AK000207	Homo sapiens	FLJ20200 fis, clone COLP1206.	2500	99
575	X52140	Rattus norvegicus	precursor polypeptide (AA -28 to 1152)	5429	87
576	AK005909	Mus musculus	putative	393	100
577	AAB08870	Homo sapiens	15-JAN-2001 03-MAR-2000 Amino acid sequence of a human secretory protein.	590	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
578	AJ296173	Mus musculus	OATS protein	582	96
580	AE003588	Drosophila melanogaster	CG13947 gene product	115	42
582	AK023117	Homo sapiens	FLJ13055 fis, clone NT2RP3001538, weakly similar to HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.	1664	99
583	BC011870	Homo sapiens	Similar to mesenchymal stem cell protein DSC43, clone MGC:19952 IMAGE:2960099, mRNA, complete cds.	1554	100
585	BC003563	Homo sapiens	guanine nucleotide binding protein (G protein), gamma 5, clone MGC:1969 IMAGE:3502879, mRNA, complete cds.	333	98
586	AL035521	Arabidopsis thaliana	putative protein	145	28
587	AY014283	Homo sapiens	mRNA, complete cds.	1066	100
588	AK020796	Mus musculus	putative	519	85
589	AL034548	Homo sapiens	DNA sequence from clone RP5-1103G7 on chromosome 20p12.2-13. Contains up to three novel genes, the gene for a novel protein similar to mouse VMP, the gene for a novel protein kinase domains containing protein similar to phosphoprotein C8FW and rat NIPK, and the SOX22 gene for SRY (sex-determining region Y)-box 22. Contains five CpG islands, ESTs, STSs and GSSs, complete sequence.	262	100
590	AK023084	Homo sapiens	FLJ13022 fis, clone NT2RP3000753, weakly similar to NEUROFILAMENT TRIPLET H PROTEIN.	1144	99
591	X97966	Homo sapiens	mRNA for calcyphosine.	963	100
592	X97966	Homo sapiens	mRNA for calcyphosine.	660	95
594	BC002471	Homo sapiens	complexin 1, clone MGC:3097 IMAGE:3349779, mRNA, complete cds.	668	99
596	BC007394	Homo sapiens	clone MGC:16291 IMAGE:3834089, mRNA, complete cds.	217	85
598	X85738	Bos taurus	novel brain-specific protein	326	55
600	AJ310530	Homo sapiens	for SMC5 protein.	880	97
601	BC001466	Homo sapiens	ring-box 1, clone MGC:1481 IMAGE:3138751, mRNA, complete cds.	131	100
602	AK012283	Mus musculus	putative	1711	96
603	AF251062	Homo sapiens	binding protein mRNA, complete cds.	1551	99
605	AAG02234	Homo sapiens	06-OCT-2000 21-FEB-2000 Human secreted protein, SEQ ID NO: 6315.	284	93
606	AAG01931	Homo sapiens	06-OCT-2000 21-FEB-2000 Human secreted protein, SEQ ID NO: 6012.	159	73
608	AK001757	Homo sapiens	FLJ10895 fis, clone NT2RP4002905.	1300	100
610	U20897	Homo sapiens	clone 475/1 melanoma ubiquitous mutated protein (MUM-1) mRNA, partial cds.	2133	100
611	AE003859	Xylella fastidiosa 9a5c	hypothetical protein	108	39
612	AK002185	Homo sapiens	FLJ11323 fis, clone PLACE1010362, weakly similar to 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10).	451	33
614	AAB41980	Homo sapiens	08-FEB-2001 31-MAR-2000 Human ORFX ORF1744 polypeptide sequence SEQ ID	116	76

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			NO:3488.		
615	AF161345	Homo sapiens	mRNA, partial cds.	439	100
616	AF116694	Homo sapiens	PRO2219	351	88
617	AAE03643	Homo sapiens	06-AUG-2001 05-DEC-2000 Human extracellular matrix and cell adhesion molecule-7 (XMAD-7).	1974	98
620	AL133640	Homo sapiens	cDNA DKFZp586C1021 (from clone DKFZp586C1021); partial cds.	2149	100
621	BC003369	Homo sapiens	ribosomal protein, large, P1, clone MGC:5215 IMAGE:2900846, mRNA, complete cds.	161	76
622	BC012124	Homo sapiens	clone MGC:20188 IMAGE:4564707, mRNA, complete cds.	810	100
625	AK008513	Mus musculus	putative	440	50
626	M32639	Homo sapiens	salivery statherin gene, exons 2-6.	276	87
627	BC008282	Homo sapiens	Similar to SH3-domain binding protein 1, clone MGC:10501 IMAGE:3639782, mRNA, complete cds.	897	96
628	AAG04000	Homo sapiens	06-OCT-2000 21-FEB-2000 Human secreted protein, SEQ ID NO: 8081.	515	100
629	AC011473	Homo sapiens	19, BAC BC349142 (CTC-518B2), complete sequence.	1392	100
632	AAY82615	Homo sapiens	02-AUG-2000 12-OCT-1998 Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.	768	88
633	AAB15539	Homo sapiens	28-FEB-2001 04-APR-2000 Human immune system molecule from Incyte clone 2907049.	637	98
634	AC018513	Homo sapiens	14 clone RP11-58H3 map 14q31, complete sequence.	818	100
635	X03249	Bos taurus	epsilon-4 beta-globin	321	79
636	AB046099	Macaca fascicularis	unnamed protein product	395	88
637	AC006033	Homo sapiens	clone RP11-121A8 from 7p14-p13, complete sequence.	1017	95
638	BC009488	Homo sapiens	Similar to CG10958 gene product, clone MGC:16372 IMAGE:3929220, mRNA, complete cds.	848	99
639	AL359620	Homo sapiens	cDNA DKFZp762P2111 (from clone DKFZp762P2111).	615	100
640	AB003184	Homo sapiens	for ISLR, complete cds.	880	59
641	AB036921	Pagrus major	maturation-inducing protein	797	69
643	AF284422	Homo sapiens	outrunner-interacting protein mRNA, complete cds.	4694	100
646	AE000659	Homo sapiens	receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.	577	100
648	AAR59748	Homo sapiens	13-FEB-1995 14-DEC-1992 T cell receptor Valpha2.3 chain.	636	100
649	AJ004871	Homo sapiens	for TCR alpha chain, specific for Mage 3/HLA-A2.	1328	94
650	AF043179	Homo sapiens	cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds.	1286	92
651	AAQ74462	Homo sapiens	03-SEP-2001 28-SEP-2000 Human colon cancer antigen protein SEQ ID NO:5226.	143	75
652	AAE02633	Homo sapiens	06-AUG-2001 03-NOV-2000 Human gene 1 encoded uteroglobin-like protein from cDNA	287	98

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			clone HTELR92.		
654	AAY70457	Homo sapiens	21-JUN-2000 02-SEP-1999 Human membrane channel protein-7 (MECHP-7).	1425	97
655	AJ406931	Homo sapiens	for keratin associated protein 3.1 (KRTAP3.1 gene).	598	100
656	AK000366	Homo sapiens	FLJ20359 fis, clone HEP16626.	2151	100
657	AF116688	Homo sapiens	PRO2133	370	98
658	BC002505	Homo sapiens	small nuclear ribonucleoprotein polypeptide F, clone MGC:1615 IMAGE:3051263, mRNA, complete cds.	222	84
659	D87009	Homo sapiens	lambda gene locus DNA, clone:288A10.	1822	99
660	AK000349	Homo sapiens	FLJ20342 fis, clone HEP13572.	3028	99
661	AK010756	Mus musculus	putative	653	84
662	AE006360	Lactococcus lactis subsp. lactis	HYPOTHETICAL PROTEIN	287	34
663	AC004832	Homo sapiens	clone RP4-539M6 from 22, complete sequence.	220	100
664	AB037902	Homo sapiens	AKR mRNA for truncated aldo-keto reductase type A, complete cds.	670	100
665	AF060511	Homo sapiens	010b10 My016 protein mRNA, complete cds.	133	52
666	M33014	Drosophila melanogaster	ubiquitin	153	62
667	AK022128	Homo sapiens	FLJ12066 fis, clone HEMBB1002266, moderately similar to NEURONAL PROTEIN.	1397	100
669	AL137512	Homo sapiens	cDNA DKFZp564E0178 (from clone DKFZp564E0178); partial cds.	751	100
670	S68015	human, mRNA, 1020 nt). [Homo sapiens		1664	100
671	U89336	Homo sapiens	class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.	2133	100
672	U89336	Homo sapiens	class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.	2094	96
673	AL136746	Homo sapiens	cDNA DKFZp434K0512 (from clone DKFZp434K0512); complete cds.	962	94
674	AF125535	Homo sapiens	homolog mRNA, complete cds.	502	95
675	AF227130	Homo sapiens	taste receptor T2R3 gene, complete cds.	1629	100
677	AB046626	Macaca fascicularis	hypothetical protein	291	93
678	AC002077	Homo sapiens	cosmid clone LUCA17 from 3p21.3, complete sequence.	1145	100
679	AE000659	Homo sapiens	receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.	565	100
680	AAY99368	Homo sapiens	08-AUG-2000 01-SEP-1999 Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.	2034	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
682	BC000555	Homo sapiens	ribosomal protein L37a, clone MGC:1638 IMAGE:3162085, mRNA, complete cds.	187	55

TABLE 3

SEQ ID NO:	Accession No.	Description	Results*
343	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 7.061e-22 151-190 BL00895C 20.10 8.071e-22 200-236 BL00895A 12.61 1.973e-18 42-63
351	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 9.299e-10 234-251
355	BL00585	Ribosomal protein S5 proteins.	BL00585A 28.43 1.391e-40 103-155
357	PR00078	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00078B 7.45 3.250e-24 146-165 PR00078D 11.49 2.800e-21 232-250 PR00078E 10.50 6.211e-16 272-288 PR00078C 15.99 8.000e-16 173-190 PR00078A 10.38 1.000e-15 111-125
359	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-13 523-562
361	BL00970	Nuclear transition protein 2 proteins.	BL00970C 14.80 9.773e-09 70-108
362	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 9.640e-09 12-25
365	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500B 7.74 3.558e-09 396-417
367	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 1.600e-10 141-155 BL50002B 15.18 6.000e-09 42-56
368	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 1.600e-10 141-155 BL50002B 15.18 6.000e-09 42-56
369	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 4.196e-11 552-600
370	BL01238	GDA1/CD39 family of nucleoside phosphatases proteins.	BL01238C 14.36 2.080e-16 212-234 BL01238D 10.19 1.180e-12 255-269 BL01238A 11.72 5.673e-11 86-101
371	PR00679	PROHIBITIN SIGNATURE	PR00679F 8.03 7.848e-25 122-146 PR00679E 12.82 6.674e-18 97-117 PR00679D 11.91 3.739e-16 74-91 PR00679B 13.63 8.071e-16 28-48 PR00679C 14.44 7.465e-14 51-70 PR00679G 6.13 1.340e-13 157-174 PR00679A 14.03 1.295e-12 10-27
374	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.462e-11 253-272
375	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.385e-15 254-267 PD00066 13.92 2.800e-14 310-323 PD00066 13.92 7.429e-12 282-295
377	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925B 3.73 6.625e-10 12-25
378	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.071e-10 3-18
380	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.250e-10 116-128
383	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.947e-17 18-35 BL00636B 15.11 5.500e-16 46-67
384	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.947e-17 18-35 BL00636B 15.11 5.500e-16 46-67
387	BL00741	Guanine-nucleotide	BL00741B 14.27 1.333e-14 302-325

SEQ ID NO:	Accession No.	Description	Results*
		dissociation stimulators CDC24 family sign.	
388	PF00628	PHD-finger.	PF00628 15.84 9.419e-09 179-194
392	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 4.364e-09 201-222
394	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 2.350e-10 132-145
397	BL01262	Eukaryotic initiation factor 1A proteins.	BL01262 22.38 6.625e-12 25-80
402	BL00056	Ribosomal protein S17 proteins.	BL00056A 28.90 3.769e-32 116-156 BL00056B 20.86 6.727e-23 164-188
403	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 9.705e-13 296-326
409	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259C 16.40 2.459e-21 78-107 PR00259A 9.27 2.846e-18 11-35 PR00259B 14.81 2.250e-17 51-78 PR00259D 13.50 2.756e-15 221-248
412	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.385e-15 105-118 PD00066 13.92 4.462e-15 161-174 PD00066 13.92 1.600e-14 189-202 PD00066 13.92 1.500e-13 133-146 PD00066 13.92 1.500e-13 217-230 PD00066 13.92 1.000e-11 21-34 PD00066 13.92 2.957e-11 77-90
413	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.400e-10 214-231 BL00028 16.07 7.171e-09 347-364
417	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 8.057e-14 199-254 PF00791B 28.49 4.909e-11 166-221
421	BL00475	Ribosomal protein L15 proteins.	BL00475D 16.25 3.250e-19 110-152 BL00475C 13.06 3.700e-17 110-127 BL00475B 8.20 2.957e-11 36-46 BL00475A 10.62 8.560e-11 16-31
428	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-10 179-212
429	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 4.375e-17 255-281 BL01153C 13.67 1.726e-11 205-219 BL01153A 13.77 4.300e-11 135-150
431	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.	DM00984B 15.18 6.764e-17 142-197
441	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.800e-09 284-299 PR00320B 12.19 1.000e-08 146-161
443	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153A 12.98 1.667e-14 49-65 PR00153B 11.57 6.667e-12 78-91
444	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 7.429e-12 4-42
446	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935D 10.20 4.656e-14 179-196 PR00935A 10.16 2.333e-12 40-53 PR00935C 11.98 2.500e-12 118-139 PR00935B 10.58 8.714e-11 105-119
447	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.643e-13 81-100
448	PR00401	SH2 DOMAIN SIGNATURE	PR00401B 12.94 7.333e-09 115-126 PR00401D 11.55 8.579e-09 144-155
453	BL00579	Ribosomal protein L29 proteins.	BL00579B 21.99 5.065e-21 35-65
457	BL00107	Protein kinases ATP-binding	BL00107A 18.39 4.960e-13 148-179

SEQ ID NO:	Accession No.	Description	Results*
		region proteins.	BL00107B 13.31 5.154e-12 222-238
458	BL00657	Fork head domain proteins.	BL00657A 19.39 1.191e-22 101-143
461	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 3.323e-14 103-120 PF00615C 10.06 4.800e-10 180-194
463	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 6.885e-09 156-172
466	PR00358	BOMBESIN RECEPTOR SIGNATURE	PR00358F 6.58 5.200e-09 15-29
467	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 1.000e-40 45-88 PD02784A 21.09 7.750e-37 5-42 PD02784C 20.76 4.106e-09 97-143
469	BL00615	C-type lectin domain proteins.	BL00615A 16.68 2.080e-11 148-166
470	BL00615	C-type lectin domain proteins.	BL00615A 16.68 2.080e-11 175-193
475	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652B 8.50 7.207e-27 127-179 PD01652A 15.35 3.557e-17 137-173 PD01652B 8.50 6.910e-10 32-84
478	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 3.179e-12 40-95
479	PF00624	Flocculin repeat proteins.	PF00624J 9.10 7.165e-09 271-301
480	PR00603	CYTOCHROME C1 SIGNATURE	PR00603H 13.20 9.534e-09 285-301
482	BL01088	CAP protein.	BL01088F 14.83 5.404e-10 60-106
485	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 2.023e-11 45-96 BL00412D 16.54 3.204e-09 41-92 BL00412D 16.54 5.684e-09 66-117
489	BL00353	HMG1/2 proteins.	BL00353A 9.60 1.000e-40 2-51 BL00353B 11.47 1.000e-40 78-128 BL00353C 14.83 1.000e-40 128-175 BL00353A 9.60 3.661e-11 3-52
495	PF00523	Fusion glycoprotein F0.	PF00523D 11.39 7.188e-10 80-94
502	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 8.606e-11 78-112
505	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683D 13.87 9.864e-09 226-243
507	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 7.513e-17 38-74 BL01189A 14.27 5.245e-09 35-71
508	PD01094	ACID FATTY DESATURASE ENDOPLASMI.	PD01094D 7.35 7.094e-11 227-281
512	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.286e-09 353-370
513	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.286e-09 353-370
514	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.714e-16 117-148
516	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e-40 93-142 BL00951B 14.23 4.300e-31 38-69 BL00951D 13.94 1.783e-30 142-177 BL00951A 15.10 1.818e-29 2-38
517	BL00951	ER lumen protein retaining receptor proteins.	BL00951D 13.94 2.761e-30 89-124 BL00951A 15.10 1.818e-29 2-38 BL00951B 14.23 5.950e-27 38-69 BL00951C 19.35 4.493e-22 40-89
522	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 3.928e-12 176-228
526	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.714e-10 31-40
534	PD00787	SYNTHASE BIOSYNTHESIS	PD00787B 13.26 1.574e-09 91-105

SEQ ID NO:	Accession No.	Description	Results*
		TRANSFERASE.	
538	PF00632	HECT-domain (ubiquitin-transferase).	PF00632C 20.66 1.540e-20 554-586 PF00632B 18.45 8.313e-20 499-527
541	BL00478	LIM domain proteins.	BL00478B 14.79 9.679e-13 62-77 BL00478B 14.79 5.750e-12 182-197 BL00478B 14.79 6.500e-12 245-260 BL00478B 14.79 3.400e-11 123-138
543	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 6.338e-36 628-675 DM00547E 13.94 2.400e-18 387-410 DM00547C 17.30 9.486e-16 266-288 DM00547B 11.28 9.217e-15 237-251 DM00547D 11.60 4.951e-12 357-371 DM00547A 12.38 6.455e-11 216-228
545	PF00777	Sialyltransferase family.	PF00777C 18.60 5.291e-21 78-133
550	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.769e-15 459-472 PD00066 13.92 2.800e-14 206-219 PD00066 13.92 2.800e-14 234-247 PD00066 13.92 2.800e-14 347-360 PD00066 13.92 2.800e-14 431-444 PD00066 13.92 2.800e-14 487-500 PD00066 13.92 2.400e-14 375-388 PD00066 13.92 5.200e-14 319-332 PD00066 13.92 8.800e-14 403-416 PD00066 13.92 4.000e-13 150-163 PD00066 13.92 5.500e-13 515-528 PD00066 13.92 7.652e-11 262-275
553	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 8.839e-14 101-118 PF00615C 10.06 3.700e-13 178-192
555	PR00180	CELLULAR RETINALDEHYDE-BINDING PROTEIN SIGNATURE	PR00180A 10.11 1.875e-16 75-98 PR00180D 12.78 1.155e-15 233-253 PR00180B 16.42 4.493e-13 124-149 PR00180C 10.92 2.901e-12 200-222
557	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.150e-10 494-507
559	BL01172	Ribosomal protein L44e proteins.	BL01172B 14.10 1.000e-40 15-57 BL01172C 16.78 3.400e-33 63-102 BL01172A 7.78 3.520e-13 2-13
562	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 1.000e-10 83-117
563	BL00484	Thyroglobulin type-1 repeat proteins proteins.	BL00484B 9.04 6.344e-14 103-117 BL00484C 17.01 8.125e-14 123-138
565	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 9.667e-10 111-121 PF00566D 11.92 1.300e-09 153-159
566	BL00580	Ribosomal protein L32e proteins.	BL00580A 17.63 9.899e-09 14-50
569	BL00674	AAA-protein family proteins.	BL00674D 23.41 4.696e-15 599-646 BL00674B 4.46 1.333e-14 508-530 BL00674C 22.60 3.786e-14 541-584
572	BL00397	Site-specific recombinases proteins.	BL00397D 19.54 8.163e-10 279-299
575	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 1.375e-26 1143-1172 BL00242C 16.86 2.324e-23 483-513 BL00242D 13.57 5.200e-22 570-595 BL00242B 8.13 6.478e-11 394-404 BL00242A 13.80 7.000e-11 75-87 BL00242D 13.57 3.957e-10 632-657
582	BL00415	Synapsins proteins.	BL00415N 4.29 2.445e-09 386-430

SEQ ID NO:	Accession No.	Description	Results*
583	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 165-178 PD00066 13.92 5.800e-14 193-206 PD00066 13.92 9.000e-13 221-234 PD00066 13.92 1.000e-12 137-150 PD00066 13.92 5.286e-12 249-262 PD00066 13.92 9.143e-12 109-122 PD00066 13.92 2.957e-11 81-94
585	BL50058	G-protein gamma subunit profile.	BL50058 27.23 8.393e-31 35-83
587	PF00628	PHD-finger.	PF00628 15.84 6.806e-09 77-92
591	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.364e-12 65-87
592	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.364e-12 65-87
600	BL00617	RecF protein.	BL00617A 25.53 6.308e-11 61-104
603	PR00216	OSTEOPONTIN SIGNATURE	PR00216C 9.63 8.636e-09 189-215
604	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 7.660e-17 397-427
610	PF00855	PWWP domain proteins.	PF00855 13.75 7.000e-10 414-431
613	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 2.523e-10 609-634
629	BL00021	Kringle domain proteins.	BL00021B 13.33 4.240e-16 48-66
635	BL01033	Globins profile.	BL01033B 13.81 5.500e-14 38-50
638	PF00992	Troponin.	PF00992A 16.67 7.868e-09 7-42
639	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.800e-14 50-63
640	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500B 7.74 7.964e-12 182-203
641	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.143e-12 316-329 PD00066 13.92 6.192e-10 344-357
643	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 2.662e-34 82-136 PD01941B 15.02 2.246e-28 267-314 PD01941D 27.18 9.194e-19 501-550 PD01941C 19.96 6.786e-13 347-402
649	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.278e-09 79-113
650	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.200e-12 162-185
654	BL00407	Connexins proteins.	BL00407E 22.17 1.000e-40 164-209 BL00407B 14.23 7.231e-35 39-70 BL00407A 18.57 5.250e-29 2-39 BL00407C 14.61 7.097e-28 70-98 BL00407D 17.61 4.000e-25 125-155
656	PR00359	B-CLASS P450 SIGNATURE	PR00359F 24.20 4.536e-10 310-338
661	BL01064	Pyridoxamine 5'-phosphate oxidase proteins.	BL01064C 15.22 1.205e-09 307-340
664	PR00069	ALDO-KETO REDUCTASE SIGNATURE	PR00069A 16.01 1.000e-18 42-67 PR00069B 11.33 1.735e-13 102-121
665	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 9.873e-12 13-48
666	PR00348	UBIQUITIN SIGNATURE	PR00348A 7.86 8.625e-09 11-32
667	BL01052	Calponin family repeat proteins.	BL01052B 15.31 2.518e-10 511-537

SEQ ID NO:	Accession No.	Description	Results*
671	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 8.941e-23 143-165 PD02327A 8.89 1.000e-13 115-127 PD02327C 15.47 5.500e-13 209-224
672	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 8.941e-23 159-181 PD02327A 8.89 1.000e-13 115-127 PD02327C 15.47 5.500e-13 225-240
678	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE	PR00441B 16.16 4.667e-26 163-186 PR00441C 14.17 1.409e-24 192-210 PR00441A 10.69 1.375e-19 31-47

* Results include in order: Accession No., subtype, e-value, and amino acid position of the signature in the corresponding polypeptide

TABLE 4

SEQ ID NO:	Pfam Model	Description	E-value	Score
350	K_tetra	K+ channel tetramerisation domain	2.3e-31	117.6
351	zona_pellucida	Zona pellucida-like domain	2.2e-25	97.7
355	Ribosomal_S5	Ribosomal protein S5	1.7e-46	167.9
357	gpdh	Glyceraldehyde 3-phosphate dehydrogenase, NA	3.1e-144	349.8
429	Nol1_Nop2_Sun	NOL1/NOP2/sun family	4.5e-19	68.6
431	LIM	LIM domain	8.6e-32	119.1
441	WD40	WD domain, G-beta repeat	2.3e-07	37.9
443	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	5.3e-34	120.4
444	DUF25	Domain of unknown function DUF25	1.1e-11	46.9
446	Band_41	FERM domain (Band 4.1 family)	3.2e-77	242.4
447	rrm	RNA recognition motif.	1.1e-33	125.4
448	SH2	SH2 domain	1.7e-33	100.2
449	UIM	Ubiquitin interaction motif	0.00071	26.3
453	Ribosomal_L29	Ribosomal L29 protein	1.7e-15	64.9
454	NTF2	Nuclear transport factor 2 (NTF2) domain	3.2e-07	37.4
457	pkinase	Protein kinase domain	6e-40	146.1
458	Fork_head	Fork head domain	1e-28	108.8
460	PC4	Transcriptional Coactivator p15 (PC4)	2.1e-38	141.0
461	RGS	Regulator of G protein signaling domain	2.6e-45	164.0
465	COX7a	Cytochrome c oxidase subunit VIIa	2.3e-40	147.5
467	rrm	RNA recognition motif.	3.2e-15	64.0
469	lectin_c	Lectin C-type domain	5.1e-06	33.3
470	lectin_c	Lectin C-type domain	5.1e-06	33.3
475	Ig	Immunoglobulin domain	9.1e-07	26.9
478	ank	Ank repeat	3e-15	64.1
481	Zip	ZIP Zinc transporter	3.8e-31	116.9
489	HMG_box	HMG (high mobility group) box	8e-33	188.9
490	PH	PH domain	2.8e-13	52.3
494	Ulp1_C	Ulp1 protease family, C-terminal catalytic d	1.2e-11	52.1
495	Peptidase_C6	Helper component proteinase	0.0056	7.9
502	Ig	Immunoglobulin domain	2.3e-09	35.2
503	Ig	Immunoglobulin domain	9.2e-09	33.3
505	PH	PH domain	1.9e-14	56.4
507	Ribosomal_L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gadd4	8.2e-14	59.3
512	zf-C2H2	Zinc finger, C2H2 type	1.1e-10	48.9
513	zf-C2H2	Zinc finger, C2H2 type	3.2e-16	67.3
514	pktrans	Protein kinase domain	3.4e-26	98.4
516	ER_lumen_recept	ER lumen protein retaining receptor	3.5e-144	492.4
517	ER_lumen_recept	ER lumen protein retaining receptor	1.8e-88	307.3
522	EMP24_GP25L	emp24/gp25L/p24 family	6.9e-06	28.1
526	SPRY	SPRY domain	2.3e-30	114.3
538	HECT	HECT-domain (ubiquitin-transferase)	1.1e-115	397.8
540	Rhomboid	Rhomboid family	4.2e-42	153.3
541	LIM	LIM domain	2e-35	131.1
542	Glyco_transf_2	Glycosyl transferase	1.7e-25	98.1
543	SNF2_N	SNF2 and others N-terminal domain	5.9e-104	358.8
545	Glyco_transf_29	Glycosyltransferase family 29	7.3e-20	79.4
546	LysM	LysM domain	2e-06	33.3
550	zf-C2H2	Zinc finger, C2H2 type	1.1e-104	361.2
553	RGS	Regulator of G protein signaling domain	2.1e-52	186.2
554	TBC	TBC domain	7.2e-35	129.3
555	CRAL_TRIO	CRAL/TRIO domain	4.5e-47	158.6
559	Ribosomal_L44	Ribosomal protein L44	1e-48	175.3
561	TIR	TIR domain	0.063	9.9

SEQ ID NO:	Pfam Model	Description	E-value	Score
562	ig	Immunoglobulin domain	3.5e-08	31.4
563	thyroglobulin_1	Thyroglobulin type-1 repeat	1.2e-54	195.0
565	TBC	TBC domain	1.1e-54	195.0
568	zf-C2H2	Zinc finger, C2H2 type	7.1e-08	39.6
569	AAA	ATPase family associated with various cellul	2e-44	161.0

TABLE 5

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB assertion
343	1bgs		40	158	3.4e-11	0.32	1.00		N-(1-D-CARBOXYLETHYL)-L-NORVALINE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE (D, L) STEREOSPECIFIC OPINE DEHYDROGENASE; OXIDOREDUCTASE
343	1cid	A	37	198	1.7e-10	0.58	0.31		L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B;	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2 OXIDOREDUCTASE
343	1cf2	P	40	112	1.4e-06	0.54	0.82		GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE; CHAIN: P, Q, S;	OXIDOREDUCTASE OXYDOREDUCTASE
343	1dlj	A	40	333	1e-36	0.14	-0.01		UDP-GLUCOSE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE ROSSMANN FOLD, TERNARY COMPLEX, CRYSTALLOGRAPHIC DIMER
343	1ae2	A	39	91	8.3e-06	0.10	0.39		ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DEHYDROGENASE, ALCOHOL, NICOTINAMIDE COENZYME, STEROID 2 BINDING
343	1f0y	A	40	324	1.2e-43	0.31	0.10		L-3-HYDROXYACYL-COA DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE H2DH; ABORTIVE TERNARY COMPLEX
343	1fmc	A	37	135	8.3e-06	0.32	0.31		7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
343	1gzh	A	25	285	1.7e-29	0.17	-0.03		OXIDOREDUCTASE(CHOH (D)-NAD(P)+ (A)) D-	OXIDOREDUCTASE (D, L) STEREOSPECIFIC OPINE DEHYDROGENASE; OXIDOREDUCTASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB assertion
343	1hdh		19	126	1.2e-05	0.02	0.30		OXIDOREDUCTASE(CHOH (D)-NAD(A)) APO-L-LACTATE DEHYDROGENASE (E.C.1.1.1.27) LDH 4	
343	1leh	A	23	226	1.7e-08	0.34	0.23		LEUCINE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE
343	1lld	A	41	156	1.7e-06	0.17	0.18		OXIDOREDUCTASE(CHOH (D)-NAD (A)) L-LACTATE DEHYDROGENASE (E.C.1.1.1.27) (T-STATE) MUTANT 1LLD 3 WITH CYS 199 REPLACED BY SER (C199S) COMPLEX WITH NADH 1LLD 4	
343	1pgd	A	40	307	3.4e-37	0.27	0.99		6-PHOSPHOGLUCONATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 6PGDH; 6-PGDH; OXIDOREDUCTASE, CHOH(D)-NADP+(B)
343	1pjc	A	41	133	1e-09	0.36	0.60		L-ALANINE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE, NAD
343	1psd	A	18	213	5.1e-34	0.15	0.44		OXIDOREDUCTASE (NAD(A)) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PHOSPHOGLYCERATE DEHYDROGENASE) (E.C.1.1.1.95) PSD 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB assertion
343	1gpd	A	37	212	1e-21	0.09	-0.09		FORMATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SIMILAR TO THE PREVIOUSLY SOLVED FORMATE DEHYDROGENASE, 2 OXIDOREDUCTASE
343	2hmd		40	123	5.1e-06	0.01	0.07		OXIDOREDUCTASE(NAD(A)-CHOH(D)) MALATE DEHYDROGENASE (E.C.1.1.1.37) 2CMD 3	
343	2ldd	A	10	162	5.4e-18	0.23	0.59		D-LACTATE DEHYDROGENASE; 2DLD 5	OXIDOREDUCTASE (CHOH(D)-NAD(A)) D-LACTATE DEHYDROGENASE; 2DLD 7
343	2ldd	A	29	215	1e-34	0.30	0.29		D-LACTATE DEHYDROGENASE; 2DLD 5 CHAIN: A, B; 2DLD 6	OXIDOREDUCTASE (CHOH(D)-NAD(A)) D-LACTATE DEHYDROGENASE; 2DLD 7
343	3pgd		42	328	1.7e-45	0.13	0.89		OXIDOREDUCTASE (CHOH(D)-NADP(A)) 6-PHOSPHOGLUCONATE DEHYDROGENASE (6-PGDH) (E.C.1.1.1.44) 2PGD	
343	3hdh	A	36	329	8.5e-43			59.63	L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
343	3hdh	A	40	324	8.5e-43	0.15	0.23		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
343	3hdh	C	15	278	6.8e-32			75.95	L-3-HYDROXYACYL COA DEHYDROGENASE;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
348	2tbv	C	74	395	1.8e-20			59.57	VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
350	1n68		41	124	1.7e-14	-0.21	0.49		POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KV1.1
350	1n68		42	123	1.1e-24	-0.39	0.49		POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KV1.1
350	1buo	A	34	136	3.1e-17	0.47	0.87		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
350	1dsx	A	41	124	1.4e-14	-0.31	0.39		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER
350	1exb	E	39	124	1e-14	0.02	0.54		KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT
350	1qdv	A	41	124	1e-14	-0.06	0.45		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B, C;	OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
343	3hdh	C	40	317	6.8e-32	0.12	0.01		L-3-HYDROXYACYL COA DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE SCHAD; OXIDOREDUCTASE, BETA OXIDATION, SCHAD, CATALYTIC ACTIVITY: 2 L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA + NADH
345	1b3u	A	272	582	0.00016	0.12	0.39		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
345	3bct		208	639	7.2e-14	-0.10	0.06		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
346	1ar1	C	128	215	3.4e-16	0.06	-0.19		CYTOCHROME C OXIDASE; CHAIN: A, B; ANTIBODY FV FRAGMENT; CHAIN: C, D;	COMPLEX (OXIDOREDUCTASE/ANTIBODY) CYTOCHROME AA3, COMPLEX IV, FERROCYTOCHROME C, COMPLEX (OXIDOREDUCTASE/ANTIBODY), ELECTRON TRANSPORT, 2 TRANSMEMBRANE, CYTOCHROME OXIDASE, ANTIBODY COMPLEX
346	1dqf	H	128	218	3.4e-16	0.04	-0.20		IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
346	1dzf	H	130	214	1.7e-16	0.10	-0.17		ANTICANCER ANTIBODY B1; CHAIN: L, H;	IMMUNOGLOBULIN B1DSFV; MONOCLONAL ANTIBODY, ANTITUMOR, IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										INTRACELLULAR GATE, TETRAMER
350	1qdv	A	42	132	1.1e-27	-0.18	0.42		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
350	1t1d	A	41	124	1.7e-14	-0.09	0.58		POTASSIUM CHANNEL KV1.1; CHAIN: A;	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, MOLECULAR 2 APLYSIA KV1.1, PROTON TRANSPORT
350	3kvt		40	132	5.4e-24	0.34	0.96		POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING
350	3kvt		41	140	1e-16	0.37	0.98		POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING
351	1ezr	L	144	238	5.4e-20	0.42	0.40		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
351	1cvw	L	227	279	3.6e-13	0.08	0.81		COAGULATION FACTOR VIIA (LIGHT CHAIN) (DES-GLA); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN) (DES-GLA); CHAIN: H; DEGR-CK INHIBITOR (GLU-GLY-ARM); CHAIN: I;	HYDROLASE BLOOD COAGULATION, FACTOR VIIA, SERINE PROTEASE, EGF, 2 INHIBITOR, CRYSTAL STRUCTURE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
346	1lgm	H	128	214	1e-15	0.09	-0.19		IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
346	1mfa		44	220	1e-19	0.02	-0.18		IMMUNOGLOBULIN FV FRAGMENT (MURINE SB155-4) COMPLEX WITH THE TRISACCHARIDE: 1MFA 3 ALPHA-D-GALACTUSE(1-2)[ALPHA-D-ABEQUOSE(1-3)]ALPHA-1MFA 4 D-MANNOSE (P1-OME) (PART OF THE CELL-SURFACE CARBOHYDRATE 1MFA 5 OF PATHOGENIC SALMONELLA) 1MFA 6	
346	1vhp		128	214	1.2e-16	0.37	-0.18		VH-PR; CHAIN: NULL;	IMMUNOGLOBULIN NMR, VH DOMAIN, ANTIBODY, HUMAN, IMMUNOGLOBULIN
347	1cwv	A	6	464	1.8e-24			79.67	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
347	1cyg		57	411	1.4e-15	0.02	-0.09		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) 1CYG 3	
347	2tbv	C	74	395	1.8e-20			59.57	VIRUS TOMATO BUSHY STUNT VIRUS 2TBV 4	
348	1cwv	A	6	464	1.8e-24			79.67	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
348	1cyg		57	411	1.4e-15	0.02	-0.09		GLYCOSYLTRANSFERASE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
351	1emn		182	261	8.5e-20	0.46	0.34		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
351	1ext	A	122	286	1.8e-15			77.32	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
351	1ext	A	123	271	1.8e-15	0.53	0.41		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
351	1fdz	B	227	268	3.6e-13	0.61	0.16		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: B;	HYDROLASE PROTEIN-INHIBITOR COMPLEX
351	1fak	L	182	273	3.4e-15	0.41	0.80		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; SL15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
351	1kto		109	352	7.2e-15	0.11	-0.12		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
351	1kto		85	222	3.4e-13	0.03	0.06		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
351	1ncf	A	121	260	3.6e-12			73.83	TUMOR NECROSIS	SIGNALLING PROTEIN TYPE I

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
351	1dan	L	124	234	5.4e-18	-0.17	0.01		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
351	1dan	L	159	268	1.8e-22	0.18	0.17		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
351	1dan	L	182	273	3.4e-15	0.57	0.87		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
351	1dva	L	179	268	7.2e-19	-0.07	0.43		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
351	1dva	L	182	273	3.4e-15	0.64	0.59		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN:	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	RECEPTOR, STNFR1; INCF 6 BINDING PROTEIN, CYTOKINE INCF 19
351	1pfx	L	101	180	5.1e-12	-0.17	0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
351	1pfx	L	103	208	5.4e-10	-0.15	0.04		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
351	1pfx	L	143	283	1.6e-20			77.38	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
351	1pfx	L	155	276	1.6e-20	0.09	0.13		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
351	1dx5	I	106	221	1.2e-17	-0.14	0.51		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
351	1dx5	I	151	257	5.1e-15	0.16	0.07		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
351	1dx5	I	151	262	5.4e-20	0.47	0.17		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
351	1emn		141	216	1.2e-17	-0.00	-0.07		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBOSOMAL PROTEIN S9; CHAIN: I; 30S RIBOSOMAL PROTEIN S10; CHAIN: J; 30S RIBOSOMAL PROTEIN S11; CHAIN: K; 30S RIBOSOMAL PROTEIN S12; CHAIN: L; 30S RIBOSOMAL PROTEIN S13; CHAIN: M; 30S RIBOSOMAL PROTEIN S14; CHAIN: N; 30S RIBOSOMAL PROTEIN S15; CHAIN: O; 30S RIBOSOMAL PROTEIN S16; CHAIN: P; 30S RIBOSOMAL PROTEIN S17; CHAIN: Q; 30S RIBOSOMAL PROTEIN S18; CHAIN: R; 30S RIBOSOMAL PROTEIN S19; CHAIN: S; 30S RIBOSOMAL PROTEIN S20; CHAIN: T; 30S RIBOSOMAL PROTEIN THX; CHAIN: V	
353	1pkp		98	253	1.4e-49	0.37	0.19		RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	
355	1pkp		98	253	1.4e-49			51.18	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	
357	3gpd	R	2	337	0			477.74	OXIDOREDUCTASE (/NADS(A)-ALDEHYDE(D))	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
351	1pfx	L	182	276	3.4e-17	0.34	0.93		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
351	1qfk	L	155	236	7.2e-20	0.13	0.29		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
351	1qfk	L	185	263	5.4e-21	-0.05	0.83		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
351	1qfk	L	186	273	1e-13	0.52	0.93		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
351	1kla	L	186	271	5.1e-15	0.38	0.48		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
357	3gpd	R	3	337	0	0.90	1.00		OXIDOREDUCTASE (/NADS(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
359	1bor		524	568	1.8e-09	-0.73	0.21		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
359	1chc		524	567	1.8e-07	-0.18	0.31		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
359	1cho		527	566	0.00034	-0.24	0.28		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
359	1ee4	A	188	328	1.6e-05	0.06	0.28		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
359	1fbv	A	492	565	5.4e-07	-0.87	0.04		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
351	9wga	A	109	250	5.4e-15	0.21	-0.13		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
351	9wga	A	124	291	1e-18	0.04	0.00		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
351	9wga	A	42	200	5.1e-24	0.07	0.40		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
351	9wga	A	9	160	1.2e-17	0.05	-0.06		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
355	1ig	B	101	263	6.8e-44	-0.06	0.18		16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER RNA; CHAIN: X; 30S RIBOSOMAL PROTEIN S2; CHAIN: B; 30S RIBOSOMAL PROTEIN S3; CHAIN: C; 30S RIBOSOMAL PROTEIN S4; CHAIN: D; 30S RIBOSOMAL PROTEIN S5; CHAIN: E; 30S RIBOSOMAL PROTEIN S6; CHAIN: F; 30S RIBOSOMAL PROTEIN S7; CHAIN: G; 30S RIBOSOMAL PROTEIN S8; CHAIN: H; 30S	RIBOSOME 30S RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, STREPTOMYCIN, 2 SPECTINOMYCIN, PAROMOMYCIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
365	1n4y	A	74	374	1.8e-46	0.18	0.99		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
365	1n9n	A	111	246	5.4e-24	0.30	0.77		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	A	128	270	5.4e-27	0.34	0.45		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	A	175	318	3.6e-25	0.55	0.68		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	A	248	390	1.8e-24	0.31	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	A	296	409	1.3e-18	0.33	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	A	90	198	1.8e-16	0.27	0.86		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	C	128	273	1.6e-27	0.48	0.59		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	C	175	318	1.8e-25	0.22	0.48		U2 RNA HAIRPIN IV;	COMPLEX (NUCLEAR PROTEIN/RNA)

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SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
359	1fbv	A	515	567	1.7e-05	-0.22	0.11		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
359	1g25	A	524	568	3.6e-07	-0.35	0.12		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
361	1elr	A	945	1046	1e-08	0.24	-0.14		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
361	1fch	A	794	1063	1.7e-08	0.07	0.04		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
361	1fch	A	942	1120	1.2e-07	0.32	0.05		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
361	1fch	A	975	1143	8.5e-11	-0.09	0.05		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
362	2bct		352	806	3.6e-17	-0.11	0.83		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN

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SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	C	272	412	1.3e-22	0.35	0.68		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1n9n	C	74	222	3.6e-17	0.16	0.23		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
365	1d0b	A	141	320	5.1e-24	0.50	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1d0b	A	16	152	8.5e-21	0.58	0.62		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1d0b	A	213	350	6.8e-24	0.70	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1d0b	A	216	417	6.8e-22	0.48	0.76		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1d0b	A	48	224	8.5e-25	0.42	0.31		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1d0b	A	93	272	1e-24	0.44	0.93		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
365	1dce	A	48	157	1.4e-11	0.59	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA

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SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
363	1cii		40	632	3.4e-10			103.86	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
363	1cun	A	37	251	1.4e-12	-0.18	0.48		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
363	1sig		71	321	7.2e-09	-0.40	0.05		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
365	1n4y	A	189	543	1.7e-17	0.06	-0.02		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
365	1n4y	A	219	395	1.3e-20	-0.01	0.42		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
365	1n4y	A	25	431	1.8e-46			70.86	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
365	1n4y	A	31	349	8.5e-16	0.15	0.39		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS

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SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
367	1azs	A	2	57	1.4e-17	0.21	1.00		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
367	1fmk		107	161	1.8e-06	0.16	0.55		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
367	1gbq	A	271	327	1.8e-19	0.74	0.95		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
367	1gbq	A	2	53	7.2e-17	-0.00	0.98		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
367	1gbr	A	271	329	1.3e-18	-0.16	0.99		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	SUBUNIT, BETA SUBUNIT
365	1dce	A	76	205	6.8e-10	0.41	0.49		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
365	1ds9	A	187	343	1.7e-13	-0.48	0.03		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
365	1ds9	A	61	223	1.7e-11	0.10	0.15		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
365	1fqv	A	220	503	8.5e-12	-0.08	0.06		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
365	1fqv	A	48	290	1.5e-15	0.05	-0.18		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
365	1fs2	A	27	246	5.1e-14	0.21	0.07		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
367	1gbr	A	94	161	3.6e-17	0.43	0.94		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
367	1gfc		101	155	1.8e-18	0.73	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
367	1gfc		4	58	1.4e-18	-0.21	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
367	1gri	A	101	330	1.3e-26			99.95	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
367	1gri	A	102	327	1.3e-26	0.25	0.81		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
367	1gri	A	4	59	1.7e-16	0.01	1.00		GROWTH FACTOR BOUND	SIGNAL TRANSDUCTION ADAPTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
365	1yrg	A	67	206	1.3e-16	0.21	0.01		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-, 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
365	2bnh		189	543	1.7e-22	0.20	-0.05		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
365	2bnh		1	431	3.6e-60			81.85	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
365	2bnh		31	395	1.7e-20	0.03	0.17		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
365	2bnh		90	401	3.6e-60	0.46	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
367	1auw		266	328	3.6e-16	0.20	0.41		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
367	1azs	A	272	325	3.6e-18	0.26	0.92		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
367	1sem	A	271	323	1.8e-17	0.11	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
367	1sem	A	4	56	7.2e-18	0.09	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
367	1sem	A	4	56	8.5e-18	0.09	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
367	1tuc		114	161	7.2e-16	0.41	0.51		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
367	1tuc		283	338	1.4e-14	-0.16	0.75		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
367	4hck		101	155	9e-17	0.19	0.59		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
368	1sww		266	328	3.6e-16	0.20	0.41		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
368	1azz	A	272	325	3.6e-18	0.26	0.92		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
368	1azz	A	2	57	1.4e-17	0.21	1.00		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
368	1fmk		107	161	1.8e-06	0.16	0.55		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
368	1gbq	A	271	327	1.8e-19	0.74	0.95		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
368	1gbq	A	2	53	7.2e-17	-0.00	0.98		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
368	1ghr	A	271	329	1.3e-18	-0.16	0.99		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SH2, SH3 1GRI 14
367	1gri	A	70	155	1.3e-17	0.08	0.42		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
367	1hsq		101	158	1.3e-16	0.17	1.00		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
367	1hsq		266	328	1.8e-16	0.20	0.55		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
367	1hsq		270	333	0.00017	-0.30	0.62		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
367	1hsq		4	61	7.2e-17	0.37	1.00		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
367	1pht		102	161	3.6e-13	0.47	0.25		PHOSPHATIDYLINOSITOL	PHOSPHOTRANSFERASE PI3K SH3;

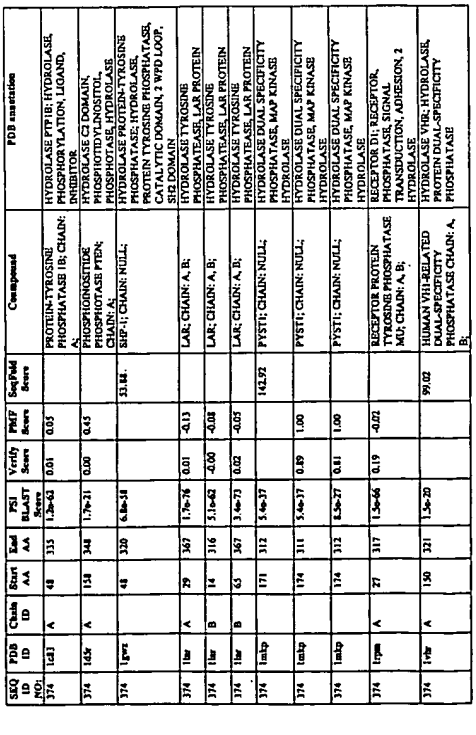
SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									3-KINASE P85-ALPHA SUBUNIT; 1PHT 6 CHAIN: NULL; 1PHT 7	1PHT 9 PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT, SH3 DOMAIN 1PHT 21
367	1pht		271	342	1.6e-15	-0.02	0.17		PHOSPHATIDYLINOSITOL 3-KINASE P85-ALPHA SUBUNIT; 1PHT 6 CHAIN: NULL; 1PHT 7	PHOSPHOTRANSFERASE PI3K SH3; 1PHT 9 PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT, SH3 DOMAIN 1PHT 21
367	1pnj		101	161	1.1e-12	0.42	0.05		PHOSPHOTRANSFERASE PHOSPHATIDYLINOSITOL 3-KINASE (P85-ALPHA SUBUNIT, 1PNJ 3 SH3 DOMAIN) (NMR, MINIMIZED AVERAGE STRUCTURE) 1PNJ 4	
367	1pwt		101	155	1.6e-18	0.80	0.82		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
367	1pwt		4	56	1.6e-18	0.25	1.00		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
367	1qkw	A	100	155	1.1e-18	0.60	0.60		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
367	1qkw	A	269	326	5.4e-18	0.42	0.99		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
367	1qkw	A	4	56	1.8e-18	0.19	0.99		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
367	1qly	A	101	155	1.4e-17	0.43	0.87		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
367	1sem	A	101	156	1.4e-17	1.29	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									STRUCTURE) 1HSQ 4	
368	1phz		102	161	3.6e-13	0.47	0.25		PHOSPHATIDYLINOSITOL 3-KINASE P85-ALPHA SUBUNIT; 1PHT 6 CHAIN: NULL; 1PHT 7	PHOSPHOTRANSFERASE PI3K SH3; 1PHT 9 PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT, SH3 DOMAIN 1PHT 21
368	1phz		271	342	1.6e-15	-0.02	0.17		PHOSPHATIDYLINOSITOL 3-KINASE P85-ALPHA SUBUNIT; 1PHT 6 CHAIN: NULL; 1PHT 7	PHOSPHOTRANSFERASE PI3K SH3; 1PHT 9 PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT, SH3 DOMAIN 1PHT 21
368	1pnj		101	161	1.1e-12	0.42	0.05		PHOSPHOTRANSFERASE PHOSPHATIDYLINOSITOL 3-KINASE (PI3-ALPHA SUBUNIT, 1PNJ 5 SH3 DOMAIN) (NMR, MINIMIZED AVERAGE STRUCTURE) 1PNJ 4	
368	1pwt		101	155	1.6e-18	0.80	0.82		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
368	1pwt		4	56	1.6e-18	0.25	1.00		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
368	1qkw	A	100	155	1.1e-18	0.60	0.60		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
368	1qkw	A	269	326	5.4e-18	0.42	0.99		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
368	1qkw	A	4	56	1.8e-18	0.19	0.99		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
368	1qfy	A	101	155	1.4e-17	0.43	0.87		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN

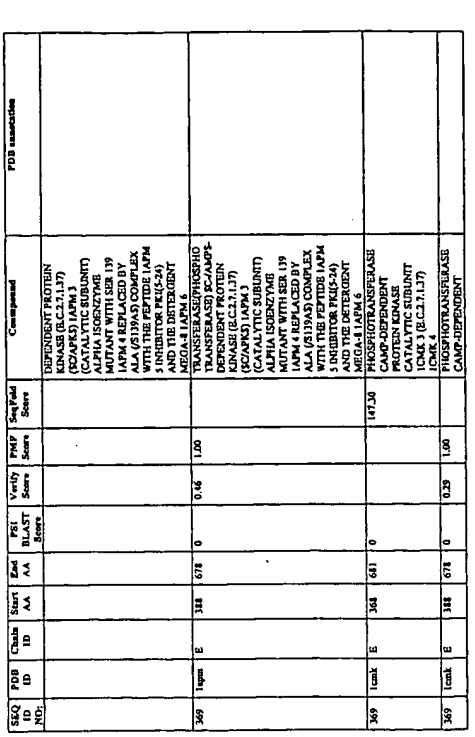
SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
368	1gbr	A	94	161	3.6e-17	0.43	0.94		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
368	1gfc		101	155	1.8e-18	0.73	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
368	1gfc		4	58	1.4e-18	-0.21	1.00		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
368	1gri	A	101	330	1.3e-26			99.95	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
368	1gri	A	102	327	1.3e-26	0.25	0.81		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN:	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
368	1scm	A	101	156	1.4e-17	1.29	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
368	1scm	A	271	323	1.8e-17	0.11	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
368	1scm	A	4	56	7.2e-18	0.09	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
368	1scm	A	4	56	8.5e-18	0.09	1.00		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
368	1tuc		114	161	7.2e-16	0.41	0.51		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
368	1tuc		283	338	1.4e-14	-0.16	0.75		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
368	4hck		101	155	9e-17	0.19	0.59		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
369	1apm	B	378	681	0			140.90	TRANSFERASE(PHOSPHO TRANSFERASE) 5C-/AMP5-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									A, B; 1GRI 6	
368	1gri	A	4	59	1.7e-16	0.01	1.00		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
368	1gri	A	70	155	1.3e-17	0.08	0.42		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
368	1hsq		101	158	1.3e-16	0.17	1.00		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
368	1hsq		266	328	1.8e-16	0.20	0.55		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
368	1hsq		270	333	0.00017	-0.30	0.62		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
368	1hsq		4	61	7.2e-17	0.37	1.00		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN	



SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	PDB annotation
374	1d1f	A	48	335	1.2e-83	0.01	0.05		PROTEIN-TYROSINE PHOSPHATASE 1B; HYDROLASE, PHOSPHORYLATION, LIGAND, INHIBITOR
374	1d5r	A	158	348	1.7e-21	0.00	0.45		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;
374	1gwz		48	320	6.8e-58			53.84	HYDROLASE C2 DOMAIN, PHOSPHOTASE, HYDROLASE PROTEIN-TYROSINE PHOSPHATASE, CATALYTIC DOMAIN, 2 WPD LOOP, SH2 DOMAIN
374	1hr	A	29	367	1.7e-78	0.01	-0.13		HYDROLASE TYROSINE
374	1hr	B	14	316	5.1e-62	-0.00	-0.01		PHOSPHATASE, LAR PROTEIN
374	1hr	B	63	367	3.4e-73	0.02	-0.05		HYDROLASE TYROSINE PHOSPHATASE, LAR PROTEIN
374	1nlp		171	312	5.4e-37			142.92	PYST1; CHAIN: NULL;
374	1nlp		174	311	5.4e-37	0.89	1.00		PYST1; CHAIN: NULL;
374	1nlp		174	312	8.5e-37	0.81	1.00		PYST1; CHAIN: NULL;
374	1ypn	A	27	317	1.5e-66	0.19	-0.02		RECEPTOR PROTEIN TYROSINE PHOSPHATASE MU; CHAIN: A, B;
374	1yhr	A	150	321	1.5e-20			99.02	HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;



SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
369	1qpm	E	388	678	0	0.46	1.00		TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAMP) (CTP 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
369	1cmk	E	368	681	0			147.50	TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAMP) (CTP 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
369	1cmk	E	388	678	0	0.29	1.00		PHOSPHOTRANSFERASE CAMP-DEPENDENT	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
374	1yhr	A	153	319	1.5e-20	0.81	1.00		HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
374	1yfo	A	23	318	5.1e-67	0.10	-0.04		RECEPTOR PROTEIN TYROSINE PHOSPHATASE ALPHA; CHAIN: A, B;	HYDROLASE D1; HYDROLASE, SIGNAL TRANSDUCTION, RECEPTOR, GLYCOPROTEIN, 2 PHOSPHORYLATION, SIGNAL
374	1ytn		217	321	1.1e-06	-0.35	0.01		YERSINIA PROTEIN TYROSINE PHOSPHATASE; CHAIN: NULL;	HYDROLASE YOP51, YOPEB, PASTEURELLA X, PTP-ASE, PROTEIN TYROSINE PHOSPHATASE, HYDROLASE
374	2ibp	A	23	317	1.7e-61	0.01	-0.03		SHP-2; CHAIN: A, B;	TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASES, INSULIN SIGNALING, SH2 PROTEIN
375	1a1b	A	213	286	1.2e-25	0.30	0.70		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
375	1aay	C	184	286	1.3e-44	-0.09	0.34		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
375	1aay	C	233	314	3.4e-31	0.47	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
375	1aay	C	261	342	1e-31	0.15	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
369	1cdp	E	374	681	0			149.99	TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAMP) (CTP 3 (CATALYTIC SUBUNIT) (CTP 4	
369	1cdp	E	388	678	0	0.36	1.00		TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAMP) (CTP 3 (CATALYTIC SUBUNIT) (CTP 4	
369	1f3m	A	15	81	3.4e-31	-0.16	0.06		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
369	1f3m	C	386	678	1.4e-95	0.65	1.00		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
374	1a5y		48	323	1e-57	0.33	0.28		PROTEIN TYROSINE PHOSPHATASE 1B; CHAIN: NULL;	HYDROLASE HYDROLASE, DEPHOSPHORYLATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLI1; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
379	1udb		27	61	0.0013	-0.86	0.01		UDP-GALACTOSE-4-EPIMERASE; CHAIN: NULL;	ISOMERASE EPIMERASE; UDP-GALACTOSE, EPIMERASE, ISOMERASE
380	1ckl	A	35	154	5.4e-30	0.45	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
380	1ckl	A	35	155	5.4e-30			91.85	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
380	1ckl	A	35	156	5.1e-29	0.54	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
380	1c5g	A	33	154	1.2e-26	0.12	0.36		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
380	1c5g	A	96	173	8.5e-17	0.06	-0.01		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, O;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
375	1mey	C	261	343	1e-51			100.95	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, O;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
375	1mey	C	289	348	1.7e-37	0.34	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, O;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
375	1tf6	A	185	323	3.4e-31	-0.23	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
375	1tf6	A	203	348	6.8e-32			66.72	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
375	1tf6	A	213	344	6.8e-32	0.10	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
375	1ubd	C	209	314	1e-31	0.34	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
380	1hfh		32	153	3.4e-34	0.54	0.43		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
380	1hfh		33	153	3.4e-24			68.71	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
380	1quh	A	2	160	3.4e-26	0.01	0.10		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
380	1quh	A	33	161	5.1e-31	0.39	0.78		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
380	1vvc		33	154	1.7e-25	0.23	0.96		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
380	1vvc		33	155	1.7e-25			67.44	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
380	1vvc		96	172	1.7e-14	-0.17	0.21		VACCINIA VIRUS COMPLEMENT CONTROL	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DNA; CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
375	1ubd	C	233	343	9e-55			85.44	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
375	1ubd	C	238	342	9e-55	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
375	1ubd	C	241	342	5.1e-34	0.38	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
375	2gli	A	201	344	1.4e-54			84.81	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
375	2gli	A	213	341	1.7e-32	0.19	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
375	2gli	A	236	348	1.4e-54	0.32	0.98		ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
384	1bq0		1	76	1.7e-23			65.24	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
384	1bq0		3	77	1.7e-23	0.90	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
384	1cun	A	165	354	7.2e-10	0.33	0.30		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
384	1ez3	A	197	306	1.6e-06	0.22	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
384	1hdj		2	76	1.8e-28	0.45	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
384	1hdj		2	76	1.8e-28			68.95	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
384	1hdj		2	77	8.5e-23	0.79	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
384	1quu	A	156	398	3.6e-07			69.36	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
384	1sig		226	386	5.4e-06	-0.07	0.03		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
384	1bq0		3	76	1e-24	0.84	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
384	1cun	A	165	354	7.2e-10	0.33	0.30		ALPHA SPECTRIN; CHAIN:	STRUCTURAL PROTEIN TWO

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									A, B, C;	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
384	1ez3	A	197	306	1.6e-06	0.22	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
384	1hdj		2	71	3.4e-23	0.68	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
384	1hdj		2	76	1.8e-28	0.45	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
384	1quu	A	156	399	1.8e-14			76.90	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
384	1sig		226	404	7.2e-07	0.07	0.01		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
385	1byr	A	131	294	7.2e-22	0.25	0.95		ENDONUCLEASE; CHAIN: A;	ENDONUCLEASE ENDONUCLEASE, PHOSPHODIESTERASE,
385	1byr	A	131	303	1.7e-21	-0.29	0.47		ENDONUCLEASE; CHAIN: A;	ENDONUCLEASE ENDONUCLEASE, PHOSPHODIESTERASE,
386	1chd	A	35	78	0.0036	0.69	0.19		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
386	1chd	A	43	88	5.4e-05	1.08	0.09		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
386	1eis	A	43	88	3.6e-05	1.00	0.00		AGGLUTININ ISOLECTIN V/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
386	1em2	A	43	88	3.6e-05	1.12	0.00		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
381	1dnl	B	155	404	0.00054	-0.22	0.09		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
383	1avl	A	148	341	7.2e-08			64.61	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
383	1bq0		1	76	1.7e-23			65.24	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
383	1bq0		3	77	1.7e-23	0.90	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
383	1cun	A	165	354	7.2e-10	0.33	0.30		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
383	1ez3	A	197	306	1.6e-06	0.22	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
383	1hdj		2	76	1.8e-28	0.45	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
383	1hdj		2	76	1.8e-28			68.95	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
383	1hdj		2	77	8.5e-23	0.79	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
383	1quu	A	156	398	3.6e-07			69.36	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
383	1sig		226	386	5.4e-06	-0.07	0.03		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
383	1bq0		3	76	1e-24	0.84	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
383	1cun	A	165	354	7.2e-10	0.33	0.30		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
383	1ez3	A	197	306	1.6e-06	0.22	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
383	1hdj		2	71	3.4e-23	0.68	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
383	1hdj		2	76	1.8e-28	0.45	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
383	1quu	A	156	399	1.8e-14			76.90	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
383	1sig		226	404	7.2e-07	0.07	0.01		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
384	1avl	A	148	341	7.2e-08			64.61	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									3 FACTOR	
394	1bd8		12	191	5.1e-30	0.07	0.96		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
394	1bd8		5	191	5.1e-30			53.62	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
394	1bi7	B	47	190	1.2e-20	-0.42	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
394	1bi8	B	12	191	1.5e-29	0.35	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
394	1bi8	B	3	161	1.5e-29			55.99	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
394	1bu9	A	34	190	1.2e-31			60.78	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
394	1bu9	A	9	188	1.2e-31	0.09	0.98		CYCLIN-DEPENDENT KINASE 6 INHIBITOR;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									V/ CHAIN: A;	SUPERANTIGEN, SACCHARIDE BINDING
388	1ciu		236	438	3.6e-08	0.11	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE ; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
388	1cwv	A	223	437	1.8e-09	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
388	1cwv	A	265	437	3.6e-11	0.34	-0.18		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
388	1qun	B	265	442	5.4e-14	0.14	-0.14		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
388	1zbd	B	162	232	0.0072	-0.41	0.25		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
388	2hap	C	161	198	0.0072	-0.44	0.31		CYC7 DNA DUPLEX; CHAIN: A, B; HEME ACTIVATOR PROTEIN; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) UAS CYC7; HAP1.18; COMPLEX (TRANSCRIPTION FACTOR/DNA), ASYMMETRY, 2 TRANSCRIPTIONAL ACTIVATION, HYPERACTIVE MUTANT
388	2vsg	A	265	440	5.4e-09	0.02	-0.19		VARIANT SURFACE GLYCOPROTEIN ILTAT 1.24; CHAIN: A, B;	MEMBRANE PROTEIN VSG VSG, TRYPANOSOME, ANTIGENIC VARIATION, MEMBRANE PROTEIN
393	1dgt	B	493	527	0.001	-0.70	0.22		DNA LIGASE; CHAIN: A, B;	LIGASE AMP COMPLEX, NAD+-DEPENDENT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A;	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
394	1d9a	A	33	190	3.6e-25	-0.25	0.59		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
394	1d9a	A	47	190	1.2e-20	-0.03	0.72		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
394	1dcq	A	10	169	1.4e-20	0.00	0.76		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
394	1dcq	A	48	191	6.8e-21	0.31	0.98		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
394	1ihb	A	41	190	1.2e-31			62.01	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
394	1ikn	D	2	76	1.7e-17	-0.16	0.78		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
394	1ikn	D	6	191	1.5e-35			54.22	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
394	1myo		10	139	3.4e-19	0.10	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
394	1myo		41	175	9e-28	-0.44	0.12		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
394	1a5e		47	190	1.4e-19	-0.02	0.87		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE/ CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
394	1awc	B	44	188	5.1e-37	0.41	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
394	1awc	B	5	188	5.1e-37			62.84	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
394	1awc	B	8	188	7.2e-32	-0.16	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
394	1awc	B	9	154	3.4e-28	0.53	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A;	HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
403	1ctl		458	519	3.6e-13	0.29	0.66		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
403	1cxx	A	464	522	7.2e-13	0.45	0.87		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
403	1dxx	A	134	383	1.5e-36	-0.01	0.18		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN
403	1lmf		466	519	1.6e-12	0.16	0.77		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
403	1qag	A	140	382	1.2e-32	0.15	0.83		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
403	1zfz		464	491	3.6e-06	-0.16	0.41		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
405	1eap	B	131	205	0.0036	0.36	0.05		CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] 1EAP 3 PHOSPHONATE 1EAP 4	
408	1fsu		21	343	3.4e-37	0.27	-0.07		N-	HYDROLASE ARYLSULFATASE B,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
394	1myo		45	188	1.5e-22	-0.28	0.49		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
394	1myo		8	151	3.6e-21	-0.21	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
394	1nfi	E	2	76	1.7e-17	-0.35	0.92		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
394	1nfi	E	4	191	8.5e-36			68.62	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
394	1nfi	E	9	187	8.5e-36	0.30	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
394	1sw6	A	132	177	3.4e-07	-0.26	0.81		REGULATORY PROTEIN SW16; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
394	1sw6	A	18	173	5.1e-19	-0.16	0.95		REGULATORY PROTEIN SW16; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
394	1sw6	A	8	175	3.6e-22	-0.09	0.58		REGULATORY PROTEIN SW16; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
394	1ycs	B	104	187	6.8e-20	-0.19	0.96		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ACETYLGALACTOSAMIN E-4-SULFATASE; CHAIN: NULL;	ASB, 4-SULFATASE; SULFATASE, GLYCOSAMINOGLYCAN DEGRADATION, HYDROLASE, SIGNAL, 2 GLYCOPROTEIN, LYSOSOME
410	1cfl	A	10	370	1.8e-47			83.44	ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED RHODOPSIN
410	1cfl	A	22	317	1.8e-47	-0.00	-0.18		ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED RHODOPSIN
410	1cfl	D	8	363	1.7e-54			78.07	ARRESTIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN RETINAL S-ANTIGEN, 48 KD PROTEIN; VISUAL ARRESTIN, DESENSITISATION OF THE VISUAL TRANSDUCTION 2 CASCADE, BINDING TO ACTICATED AND PHOSPHORYLATED RHODOPSIN
412	1a1h	A	2	81	8.5e-28	0.34	1.00		QUSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
412	1bft	A	24	219	7.2e-17			64.99	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
394	1ycs	B	42	190	7.2e-23	-0.53	0.19		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
403	1a7i		464	522	5.4e-13	0.26	0.72		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
403	1aon		138	376	8.5e-27	-0.05	0.93		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN-BINDING PROTEIN, CALCIUM-BINDING, PHOSPHORYLATION
403	1bft	A	432	519	1.8e-13	-0.10	0.51		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
403	1bft	A	460	519	9e-14	0.20	0.48		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
403	1bhd	A	275	375	1e-12	0.79	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
403	1bhd	A	281	379	1.8e-26	1.06	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
403	1bkr	A	278	383	6.8e-16	0.91	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
403	1bkr	A	281	383	1.1e-27	0.97	1.00		SPECTRIN BETA CHAIN;	ACTIN-BINDING CALPONIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	142	250	1.8e-58			85.17	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	148	249	6.8e-35	-0.09	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	36	137	5.1e-35	0.07	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	3	137	7.2e-41	-0.10	0.62		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	3	81	8.5e-28	-0.32	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
412	1mey	C	140	221	1e-49	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	168	249	1.7e-50	-0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	168	250	1.7e-50			99.05	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	196	260	8.5e-39	-0.05	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	28	109	1.7e-49	0.11	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	2	81	1.7e-46	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1mey	C	56	137	1e-49	0.11	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DNA; CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	54	165	3.6e-53	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	8	109	1.7e-34	0.10	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	1ubd	C	92	193	1.7e-35	0.31	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
412	2gli	A	120	248	5.1e-34	0.05	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	12	108	3.4e-31	-0.13	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	148	258	1e-29	-0.05	0.52		ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										(ZINC FINGER/DNA)
412	1mey	C	84	165	1e-49	0.36	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
412	1tf6	A	113	258	1.4e-36	-0.02	0.93		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
412	1tf6	A	29	174	5.1e-37	-0.17	0.84		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
412	1tf6	A	3	153	3.4e-37	-0.20	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
412	1tf6	A	84	251	1.8e-77			104.19	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
412	1ubd	C	138	249	1.8e-58	0.05	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										3 FACTOR
417	1awc	B	166	329	8.5e-33	0.09	0.99		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
417	1bd8		135	268	1e-31	0.31	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
417	1bd8		155	277	5.4e-35	0.45	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
417	1bd8		169	332	1.7e-25	0.11	0.40		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
417	1bd8		9	181	1.7e-20	-0.32	0.01		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
417	1bi7	B	155	248	1.8e-28	0.28	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
417	1bix	B	135	268	3.4e-32	0.32	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLI1; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	28	167	3.6e-64	0.12	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	56	195	3.6e-75			91.24	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	56	195	5.4e-71	0.15	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	5	139	9e-43	-0.57	0.80		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
412	2gli	A	84	250	3.6e-75	-0.15	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
413	1bbo		319	371	0.00014	-0.89	0.06		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
413	3znf		210	239	1.4e-10	0.20	0.76		ZINC FINGER /DNA5 BINDING DOMAIN ZINC FINGER (/NMR5) 3ZNF 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										PROTEIN/KINASE)
417	1bix	B	150	279	9e-36	0.48	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
417	1bix	B	169	332	1.7e-25	-0.07	0.78		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
417	1bu9	A	132	268	3.4e-33	0.39	0.43		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
417	1bu9	A	166	334	8.5e-30	0.03	0.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
417	1d9z	A	155	279	1.4e-35	0.47	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
417	1dcq	A	152	262	1.1e-31	0.48	1.00		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
417	1ihb	A	132	268	3.4e-33	0.38	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
413	3znf		345	371	0.0046	0.23	0.76		ZINC FINGER /DNA5 BINDING DOMAIN ZINC FINGER (/NMR5) 3ZNF 3	
413	7znf		210	238	0.00017	-0.24	0.71		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES) 7ZNF 3	
417	1a5e		155	269	1.8e-31	0.36	0.99		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
417	1awc	B	102	247	3.4e-39	0.19	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
417	1awc	B	132	267	3.4e-36	0.30	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
417	1awc	B	156	268	9e-37	0.59	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HLA6E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
417	1ibb	A	166	333	1.7e-29	0.03	0.71		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
417	1ikn	D	127	329	8.5e-36	-0.13	0.11		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
417	1myo		103	216	1.2e-23	-0.32	0.09		MYOTROPHIN; CHAIN: NULL;	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
417	1myo		133	249	1.4e-25	0.10	0.88		MYOTROPHIN; CHAIN: NULL;	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
417	1myo		155	245	1.4e-27	0.08	1.00		MYOTROPHIN; CHAIN: NULL;	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
417	1myo		163	278	1.1e-38	0.40	1.00		MYOTROPHIN; CHAIN: NULL;	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
417	1myo		200	314	6.8e-17	-0.08	0.41		MYOTROPHIN; CHAIN: NULL;	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
417	1nfi	E	126	329	1.4e-35	-0.08	0.21		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
417	1ycs	B	164	304	3.6e-33	0.22	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
417	1ycs	B	2	48	8.5e-13	0.09	-0.19		P53; CHAIN: A; 53BP2;	COMPLEX (ANTI-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
431	1a7i		104	159	1.3e-16	-0.32	0.93		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
431	1a7i		104	163	3.1e-13	-0.06	0.72		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
431	1b8r	A	97	296	3.4e-25			65.67	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
431	1ctl		166	232	8.5e-14	0.01	0.22		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
431	1ctl		226	294	3.4e-14	-0.14	0.01		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
431	1ctl		98	159	1.8e-18	-0.19	0.78		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
431	1ctl		99	159	3.4e-14	0.07	0.37		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
431	1ccx	A	105	159	3.4e-14	-0.14	0.66		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
431	1cxx	A	106	159	1.3e-16	-0.22	0.59		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
431	1iml		104	159	1.7e-13	-0.24	0.82		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
431	1iml		106	171	5.4e-17	-0.29	0.07		CYSTEINE RICH	METAL-BINDING PROTEIN CRP;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: B;	ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
419	1hx7		209	237	0.0054	-0.83	0.01		HIRUSTASIN; CHAIN: NULL;	ANTI-COAGULANT ANTI-COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR
421	1ffk	J	16	156	6.8e-21	-0.33	0.00		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L7AE; CHAIN: E; RIBOSOMAL PROTEIN L10E; CHAIN: F; RIBOSOMAL PROTEIN L13; CHAIN: G; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L13; CHAIN: J;	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4, 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 30S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 30S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
431	1iml		165	230	1.7e-13	0.08	0.18		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
431	1iml		165	235	1.8e-17	0.20	0.15		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
441	1erj	A	177	360	3.4e-33	0.14	0.28		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
441	1erj	A	17	296	1.2e-53	0.69	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
441	1erj	A	41	349	1e-50	0.70	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
441	1flg	A	205	296	0.0014	-0.29	0.12		QUINOPROTEIN ETHANOL DEHYDROGENASE; CHAIN: A, B	OXIDOREDUCTASE QUINOPROTEIN, SUPERBARREL, DEHYDROGENASE
441	1got	B	21	378	5.1e-56			67.04	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
441	1got	B	23	297	5.1e-46	0.86	0.98		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
441	1got	B	76	370	5.1e-56	0.45	0.80		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
441	1qks	A	42	300	1.3e-16	0.12	-0.15		CYTOCHROME CD1 NITRITE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE ENZYME, NITRITE REDUCTASE, OXIDOREDUCTASE, DENITRIFICATION, 2 ELECTRON TRANSPORT, PERIPLASMIC
443	1awq	A	27	113	1.7e-47	-0.02	0.92		CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
443	1awq	A	27	114	1.7e-47			72.97	CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
446	1ef1	A	15	291	8.5e-55	0.43	1.00		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
446	1ef1	A	25	290	3.6e-88	0.41	1.00		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
446	1gc7	A	15	291	3.1e-56	0.62	1.00		RADIXIN; CHAIN: A;	CELL ADHESION 3 SUBDOMAINS,CYTOSKELETON, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ADHESION
446	1gc7	A	25	290	7.2e-88	0.56	1.00		RADIXIN; CHAIN: A;	CELL ADHESION 3 SUBDOMAINS,CYTOSKELETON, CELL ADHESION
447	1b7f	A	154	311	1.7e-29	0.13	0.13		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP *UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
447	1b7f	A	77	232	1.4e-39	1.11	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP *UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
447	1b7f	A	77	232	1.4e-39			81.68	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP *UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
447	1cvj	A	155	316	1.7e-29	0.14	0.24		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	A	42	148	1.7e-31	0.71	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
447	1cvj	A	79	238	1.2e-38			79.42	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	A	80	236	1.2e-38	0.78	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	B	155	298	3.4e-27	0.17	0.74		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	B	42	135	1.5e-28	0.48	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	B	79	218	5.1e-34			72.29	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	BINDING DOMAIN
447	1snc	B	80	149	3.6e-19	0.63	1.00		RIBONUCLEOPROTEIN PROTEIN FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) 1NRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 1NRC 4 REPLACED BY CYS (Q85C) 1NRC 5	
447	1qm9	A	80	211	5.4e-22	0.16	0.95		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
447	2mss	A	154	232	6.8e-19	0.62	0.98		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
447	2up1	A	154	317	1.7e-37	0.17	0.41		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
447	2up1	A	73	238	3.4e-49	0.75	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									T;	
447	1cvj	B	80	219	5.1e-34	0.97	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	F	155	288	1.7e-23	0.25	0.65		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	F	80	204	1.7e-26	0.64	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	H	155	291	6.8e-24	0.25	0.69		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1cvj	H	42	128	1.7e-20	0.18	0.57		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3');	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
447	3sxl	A	154	311	1.4e-26	0.01	0.18		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
447	3sxl	A	78	213	5.1e-39	0.87	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
447	3sxl	A	78	223	5.1e-39			78.28	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
448	1a09	A	89	192	3.4e-24			78.11	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
448	1a09	A	93	192	3.4e-24	1.16	1.00		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
448	1a81	B	1	194	3.4e-16			52.85	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: M, N, O, P, Q, R, S, T;	
447	1cvj	H	80	207	3.4e-26	0.62	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
447	1d8z	A	76	152	3.4e-20	1.10	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
447	1fht		79	164	1.4e-18	1.00	0.99		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME
447	1fjc	A	71	149	3.6e-18	0.71	0.96		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
447	1ha1		154	311	8.5e-36	0.05	0.43		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
447	1ha1		74	232	1.4e-48	0.97	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
447	1hd1	A	154	232	1.7e-19	0.77	0.98		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
447	1hd1	A	80	149	3.4e-20	1.55	1.00		HETEROGENEOUS	RNA BINDING PROTEIN RNA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
448	1grl	A	36	180	1.5e-23	0.41	0.92		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
448	1hsq		30	97	5.1e-10	0.04	-0.13		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
448	1lck	A	34	193	1.4e-35			136.33	P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQQ(PHOSPHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
448	1lck	A	35	191	6.8e-35	0.55	1.00		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQQ(PHOSPHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
448	1lck	A	38	177	1.4e-35	0.66	1.00		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQQ(PHOSPHO)YQPQPA; 1LCK 14 CHAIN: B; 1LCK 15	COMPLEX (KINASE/PEPTIDE)
448	1llk	A	90	193	5.1e-24			95.11	HUMAN P56 TYROSINE KINASE; 1LKK 7 CHAIN: A; 1LKK 8	COMPLEX (TYROSINE KINASE/PEPTIDE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
448	1ab2		84	196	1.7e-18			56.12	TRANSFERASE(PHOSPHO TRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
448	1aot	F	88	193	1.4e-22			77.83	FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
448	1bkl		92	201	1.2e-25			85.76	PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
448	1bkl		93	196	1.2e-25	1.08	1.00		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
448	1blj		81	195	1.4e-23			90.55	P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION
448	1cwd	L	93	189	9e-24			91.11	P56LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PHOSPHOTRANSFERASE, COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
448	1efn	A	37	88	1.7e-10	-0.04	0.03		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; 1LKK 11 CHAIN: B; 1LKK 12	
448	1llk	A	93	191	5.1e-24	1.31	1.00		HUMAN P56 TYROSINE KINASE; 1LKK 7 CHAIN: A; 1LKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; 1LKK 11 CHAIN: B; 1LKK 12	COMPLEX (TYROSINE KINASE/PEPTIDE)
448	1qcf	A	37	207	1.2e-44	0.74	1.00		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
448	1sem	A	35	86	1.7e-10	0.09	0.01		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
448	1sha	A	91	193	6.8e-25			84.13	PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	
448	1sha	A	93	192	6.8e-25	1.14	1.00		PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN; CHAIN: B, D;	DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
448	1fmk		34	207	3.4e-42	0.60	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
448	1gbr	A	27	93	3.4e-10	0.01	0.23		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
448	1gfc		37	88	3.4e-10	0.25	-0.11		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
448	1grl	A	35	209	1.5e-23			50.22	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
457	1cki	A	16	324	5.4e-30			63.66	CASEIN KINASE I DELTA; ICKI 6 CHAIN: A, B; ICKI 7	PHOSPHOTRANSFERASE PROTEIN KINASE ICKI 18
457	1ckj	A	19	310	5.4e-30	0.30	0.93		CASEIN KINASE I DELTA; ICKI 6 CHAIN: A, B; ICKI 7	PHOSPHOTRANSFERASE PROTEIN KINASE ICKI 18
457	1cm8	A	17	314	2.4e-36	0.54	1.00		PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3, ERK6, ERK5; P38-GAMMA, GAMMA, PHOSPHORYLATION, MAP KINASE
457	1cmk	E	3	357	1.9e-28			84.57	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	
457	1ctp	E	1	357	8.1e-28			83.76	TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
457	1cx0	A	336	397	5.4e-09	0.26	0.71		U1A PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	RNA BINDING PROTEIN/RNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE
457	1dfz	A	345	397	5.4e-07	0.28	0.93		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
457	1fgk	A	9	311	2.7e-20			79.13	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	
448	2abl		28	189	3.4e-29			87.30	ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
448	2abl		29	192	3.4e-29	0.74	0.99		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
448	3hck		89	195	3.4e-26	0.95	1.00		HCK SH2; CHAIN: NULL;	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE
448	3hck		90	195	3.4e-26			103.54	HCK SH2; CHAIN: NULL;	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE
454	1ar0	A	12	141	2.2e-31			60.79	NUCLEAR TRANSPORT FACTOR 2; CHAIN: A, B;	TRANSPORT PP15, B2; TRANSPORT, NUCLEAR TRANSPORT PROTEIN
454	1ar0	A	18	136	2.2e-31	0.49	0.96		NUCLEAR TRANSPORT FACTOR 2; CHAIN: A, B;	TRANSPORT PP15, B2; TRANSPORT, NUCLEAR TRANSPORT PROTEIN
457	1a06		29	347	5.4e-25			69.61	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
457	1a9n	B	341	397	8.1e-09	0.42	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'';	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										RECEPTOR, PHOSPHOTRANSFERASE
457	1fgk	B	6	310	1.4e-21			81.51	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
457	1fht		341	397	1.4e-08	0.50	0.75		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME
457	1fjc	A	345	412	8.1e-07	-0.12	0.16		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
457	1hcl		22	317	8.1e-35			99.28	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
457	1hcl		23	304	8.1e-35	0.40	1.00		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
457	1ian		11	350	8.1e-25			97.38	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
457	1ir3	A	9	324	2.7e-19			74.34	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: B, D;	
457	1aq1		22	317	8.1e-33			92.24	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
457	1aq1		23	310	8.1e-33	0.37	1.00		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
457	1bi8	A	21	305	5.4e-36			76.98	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER, HELIX
457	1bi8	A	24	304	5.4e-36	0.42	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER, HELIX
457	1blx	A	16	314	2.2e-39			103.69	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
457	1blx	A	23	304	2.2e-39	0.32	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
457	1jnk		17	310	1.1e-31	0.44	0.95		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
457	1jnk		4	345	1.1e-31			95.25	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
457	1kon		1	417	8.1e-29			78.60	TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
457	1pme		20	321	1.1e-33	0.32	0.99		ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
457	1pme		20	341	1.1e-33			94.17	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
457	1qm9	A	345	397	8.1e-08	0.19	0.62		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
457	1tki	A	17	365	1.4e-29			96.61	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
457	1tki	A	74	304	1.4e-29	0.05	0.98		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
457	1urn	A	336	397	2.7e-09	0.75	0.76		U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 21MER HAIRPIN (5'-(AP*AP*UP*CP*CP*AP*UP *UP* 1URN 11 CHAIN: P, Q, R 1URN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
457	2u2f	A	345	397	8.1e-07	0.18	0.78		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
457	3erk		10	349	5.4e-34			94.87	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
457	3erk		24	321	5.4e-34	0.39	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
458	1d5v	A	100	179	8.1e-28	0.29	1.00		S12 TRANSCRIPTION FACTOR (FKH-14); CHAIN: A;	GENE REGULATION WINGED HELIX, DNA-RECOGNITION HELIX
458	1e17	A	101	173	8.1e-26	0.43	1.00		AFX; CHAIN: A;	DNA BINDING DOMAIN DNA BINDING DOMAIN, WINGED HELIX
458	2hdc	A	100	173	2.2e-28	0.27	1.00		HNF3/FH TRANSCRIPTION FACTOR GENESIS; CHAIN: A; 5'- CHAIN: B; 5'- CHAIN: C;	GENE REGULATION/DNA HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2, NMR, STRUCTURE, DYANAMICS, GENESIS, WINGED HELIX PROTEIN, 2 GENE REGULATION/DNA
458	2hdc	A	100	197	2.2e-28			79.14	HNF3/FH TRANSCRIPTION FACTOR GENESIS; CHAIN: A; 5'- CHAIN: B; 5'- CHAIN: C;	GENE REGULATION/DNA HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2, NMR, STRUCTURE, DYANAMICS, GENESIS, WINGED HELIX PROTEIN, 2 GENE REGULATION/DNA
458	2hfh		100	173	1.6e-28	0.17	1.00		GENESIS; CHAIN: NULL;	HNF-3 HOMOLOGUES HFH-2; HNF-3 HOMOLOGUES, WINGED HELIX PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
458	2hfh		99	192	1.6e-28			76.10	GENESIS; CHAIN: NULL;	HNF-3 HOMOLOGUES HFH-2; HNF-3 HOMOLOGUES, WINGED HELIX PROTEIN
460	1cr5	A	71	118	0.0054	-0.29	0.03		SEC18P (RESIDUES 22 - 210); CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS DOUBLE-PSI BETA BARREL, VESICLE FUSION, 2 ENDOCYTOSIS/EXOCYTOSIS
460	1pcf	A	62	128	5.4e-20			81.97	TRANSCRIPTIONAL COACTIVATOR PC4; CHAIN: A, B, C, D, E, F, G, H;	TRANSCRIPTION P15; TRANSCRIPTION, TRANSCRIPTIONAL COFACTOR, TRANSCRIPTIONAL 2 CO-ACTIVATOR, SSDNA BINDING, NUCLEAR PROTEIN
460	1pcf	A	63	110	5.4e-20	0.33	1.00		TRANSCRIPTIONAL COACTIVATOR PC4; CHAIN: A, B, C, D, E, F, G, H;	TRANSCRIPTION P15; TRANSCRIPTION, TRANSCRIPTIONAL COFACTOR, TRANSCRIPTIONAL 2 CO-ACTIVATOR, SSDNA BINDING, NUCLEAR PROTEIN
461	1cmz	A	75	202	2.7e-50			110.58	GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
461	1cmz	A	76	202	2.7e-50	0.54	1.00		GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
461	1dks	A	78	209	5.4e-42	0.43	0.98		AXIN; CHAIN: A;	SIGNALING PROTEIN ALPHA-HELIX, PI-HELIX
461	1emu	A	82	200	1.6e-37	0.50	1.00		AXIN; CHAIN: A; ADENOMATOUS POLYPOSIS COLI	SIGNALING PROTEIN RGS DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN; CHAIN: B;	
463	1cb9	A	5	66	0.0081	-0.44	0.35		CYTOTOXIN 2; CHAIN: A	TOXIN CYTOXIN (CARDIOTOXIN), MEMBRANE PERTURBATION, CIS/TRANS 2 ISOMERIZATION, BOUND WATER
463	1cdt	A	5	66	0.0054	0.23	0.00		CYTOTOXIN CARDIOTOXIN V=4=====IIS=== (TOXIN /IIIS) 1CDT 3	
463	1tgx	A	5	66	0.0054	-0.11	0.09		CYTOTOXIN TOXIN GAMMA (CARDIOTOXIN) 1TGX 3	
463	2abx	A	91	171	0.00081	-0.03	0.05		POSTSYNAPTIC NEUROTOXIN ALPHA-*BUNGAROTOXIN 2ABX 4	
463	2cdx		5	66	0.0054	0.00	0.01		CARDIOTOXIN CARDIOTOXIN CTX I (NMR, 11 STRUCTURES) 2CDX 3	
465	2occ	J	64	120	2.7e-20			57.62	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C\OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
465	2occ	J	73	118	2.7e-20	-0.89	0.34		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C\OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBONUCLEOPROTEIN A; CHAIN: NULL;	PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
467	2up1	A	8	174	2.4e-12	0.28	0.24		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
468	1h3u	A	222	444	0.0011	-0.15	0.15		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
469	1b08	A	100	258	1.1e-23	0.02	0.19		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
469	1b6e		134	260	3.4e-26	0.53	1.00		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
469	1b6e		134	261	5.4e-26			86.24	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
469	1c3a	B	137	261	2.7e-24	0.06	0.78		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
469	1e87	A	135	259	8.1e-26	0.55	0.87		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
467	1a9n	B	3	96	8.1e-32	1.50	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
467	1a9n	B	3	96	8.1e-32			147.88	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
467	1b7f	A	3	172	8.1e-16			59.62	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
467	1b7f	A	6	161	8.1e-16	0.18	0.92		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
467	1cvj	A	7	174	1.4e-14			54.28	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
467	1cvj	A	8	173	1.4e-14	0.42	0.86		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
467	1cvj	B	8	161	8.1e-15	0.26	0.52		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
469	1ixx	B	136	261	1.3e-23			36.80	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
469	1ixx	B	137	261	1.3e-23	0.18	0.62		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
469	1lit		137	261	1.9e-21			53.00	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
469	1qdd	A	124	261	1.4e-24			59.68	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
469	1qdd	A	134	260	1.4e-24	0.36	0.96		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
469	1qa3	C	132	260	1.4e-27	0.24	0.75		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
469	1qa3	D	141	260	2.7e-25	0.14	1.00		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
467	1cvj	P	8	149	1.9e-12	0.26	0.99		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
467	1cvj	H	8	151	8.1e-14	0.47	0.89		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
467	1hal		8	167	1.1e-10	0.41	0.78		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
467	1qm9	A	6	174	8.1e-21	-0.21	0.33		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
467	2u1a		127	174	1.9e-09	-0.11	0.99		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN U1 SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
467	2u1a		94	174	1.9e-09			64.11	U1 SMALL NUCLEAR	NUCLEAR PROTEIN U1 SNRNP A

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										LY-49
469	1qo3	D	168	287	2.7e-25	0.14	1.00		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
469	1tn3		161	285	2.7e-24	0.15	0.89		TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
469	2afp	A	159	285	3.4e-26	-0.06	0.58		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN
470	1b08	A	100	258	1.1e-23	0.02	0.19		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
470	1b6e		134	260	5.4e-26	0.53	1.00		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
470	1b6e		134	261	5.4e-26			86.24	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
470	1e3e	B	137	261	2.7e-24	0.06	0.78		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
469	1tn3		134	258	2.7e-24	0.15	0.89		TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
469	2afp	A	132	258	5.4e-26	-0.06	0.58		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN
469	1b08	A	148	285	5.4e-24	-0.05	0.25		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
469	1b6e		161	287	5.4e-26	0.53	1.00		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
469	1b6e		161	288	5.4e-26			86.29	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
469	1e3e	B	164	288	2.7e-24	0.06	0.78		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
469	1e87	A	162	286	8.1e-26	0.55	0.87		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SUBUNIT; CHAIN: B	
470	1e87	A	135	259	8.1e-26	0.55	0.87		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
470	1bxx	B	136	261	1.3e-23			36.80	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
470	1bxx	B	137	261	1.3e-23	0.18	0.62		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
470	1lit		137	261	1.9e-21			53.00	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
470	1qdd	A	124	261	1.4e-24			59.68	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
470	1qdd	A	134	260	1.4e-24	0.36	0.96		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
470	1qo3	C	132	260	1.4e-27	0.24	0.75		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
469	1bxx	A	163	286	8.1e-21			50.25	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
469	1bxx	B	163	288	1.3e-23			58.01	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
469	1bxx	B	164	288	1.3e-23	0.18	0.62		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
469	1lit		164	288	1.9e-21			54.16	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
469	1qdd	A	151	288	1.4e-24			63.08	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
469	1qdd	A	161	287	1.4e-24	0.36	0.96		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
469	1qo3	C	157	287	8.1e-28	0.41	0.72		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
470	1qo3	D	168	287	2.7e-25	0.14	1.00		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
470	1tn3		161	285	2.7e-24	0.15	0.89		TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
470	2afp	A	159	285	5.4e-26	-0.06	0.58		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN
472	1qft	A	64	328	8.1e-19	-0.09	0.57		PURPLE ACID PHOSPHATASE; CHAIN: A;	HYDROLASE TARTRATE RESISTANT ACID PHOSPHATASE, TRAP; HYDROLASE, METAL PHOSPHATASE
472	1qhw	A	70	335	5.4e-22	-0.03	0.23		PURPLE ACID PHOSPHATASE; CHAIN: A;	HYDROLASE TARTRATE-RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE
475	1hlh	A	50	220	3.4e-09	0.28	0.29		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										HISTOCOMPATIBILITY, B2M, LY49, LY-49
470	1qo3	D	141	260	2.7e-25	0.14	1.00		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
470	1tn3		134	258	2.7e-24	0.15	0.89		TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
470	2afp	A	132	258	5.4e-26	-0.06	0.58		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN
470	1b08	A	148	285	5.4e-24	-0.05	0.25		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
470	1b6o		161	287	5.4e-26	0.53	1.00		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
470	1b6e		161	288	5.4e-26			86.29	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
470	1c3a	B	164	288	2.7e-24	0.06	0.78		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
475	1cvs	C	56	162	5.4e-08	0.10	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
475	1cvs	D	56	162	5.4e-07	-0.04	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
475	1cpf	A	52	162	8.1e-07	-0.03	0.40		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
475	1evt	C	57	162	2.2e-07	0.43	0.19		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
475	1ffq	A	46	239	5.4e-23	0.46	0.96		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
475	1f6a	A	46	231	1.3e-23	0.30	0.45		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
475	1fcg	A	46	236	8.1e-29	0.32	0.99		FC RECEPTOR	IMMUNE SYSTEM, MEMBRANE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SUBUNIT; CHAIN: B	
470	1e87	A	162	286	8.1e-26	0.55	0.87		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
470	1ixx	A	163	286	8.1e-21			50.25	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
470	1ixx	B	163	288	1.3e-23			58.01	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
470	1ixx	B	164	288	1.3e-23	0.18	0.62		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
470	1lli		164	288	1.9e-21			54.16	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
470	1qdd	A	151	288	1.4e-24			63.08	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
470	1qdd	A	161	287	1.4e-24	0.36	0.96		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
470	1qo3	C	157	287	8.1e-28	0.41	0.72		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										3 FACTOR
478	1bd8		16	157	8.1e-23	0.22	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
478	1bd8		1	155	8.1e-23			56.30	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
478	1bi7	B	1	123	2.2e-21			52.64	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
478	1bi7	B	20	123	2.2e-21	0.06	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
478	1bi8	B	16	157	1.4e-24	0.01	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
478	1bi8	B	1	158	1.4e-24			56.51	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FC(GAMMA)RIIA; CHAIN: A;	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
475	1fnl	A	43	239	1.6e-28	0.41	0.54		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
475	1nkr		141	244	1.3e-28	0.51	1.00		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
475	1nkr		45	237	2.7e-68			146.01	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
475	1nkr		46	237	2.7e-68	0.72	1.00		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
475	1vca	A	45	245	1.1e-08			52.80	HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
475	1vca	A	46	195	1.1e-08	0.12	0.07		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
475	1zxq		52	162	5.4e-08	0.17	-0.05		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										PROTEIN/KINASE)
478	1bu9	A	13	123	2.4e-22	0.11	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
478	1bu9	A	1	161	2.4e-22			59.54	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
478	1d9s	A	13	124	5.4e-23	0.31	0.77		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
478	1ibb	A	13	123	1.6e-23	0.24	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
478	1ibb	A	1	159	1.6e-22			62.69	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
478	1myo		13	119	2.7e-21	0.17	0.82		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
478	1ycs	B	13	128	8.1e-21	-0.01	0.64		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
475	2dil	A	139	250	8.1e-18	0.20	1.00		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
475	2dil	A	45	256	5.4e-40	0.65	1.00		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
478	1awc	B	13	121	5.4e-23	0.38	0.99		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
478	1awc	B	13	157	1.1e-21	0.50	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
478	1awc	B	1	152	5.4e-23			61.05	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
484	1cvj	H	48	134	0.0027	0.68	0.39		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
484	1d8z	A	48	134	0.0011	0.33	0.05		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
484	2u2f	A	48	134	0.00027	0.43	0.27		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
485	1d0s	A	75	217	1.6e-09	0.13	-0.20		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
485	1req	A	16	193	2.7e-13	0.33	-0.19		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
485	1req	A	17	227	8.1e-10	0.04	-0.20		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
489	1aab		2	84	2.2e-30	1.08	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-BOX 1AAB 20
489	1aab		2	84	2.2e-30			131.01	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-BOX 1AAB 20

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ONCOGENE/ANKYRIN REPEATS)
480	2dld	A	18	111	3.4e-09	0.58	0.80		D-LACTATE DEHYDROGENASE; 2DLD 5 CHAIN: A, B; 2DLD 6	OXIDOREDUCTASE (CHOH(D)-NAD+(A)) R-LACTATE DEHYDROGENASE; 2DLD 7
482	1bc4	A	251	308	0.00054	0.02	0.89		NUCLEOSIDE DIPHOSPHATE TRANSFERASE; CHAIN: A, B, C;	PHOSPHOTRANSFERASE PHOSPHOTRANSFERASE
482	1dtw	A	251	308	0.00054	0.20	0.87		NUCLEOSIDE DIPHOSPHATE KINASE; CHAIN: A, B;	TRANSFERASE NDPK H4; NUCLEOSIDE DIPHOSPHATE KINASE, NM23, MITOCHONDRIAL, KILLER- 2 OF-PRUNE
482	1nhk	R	250	308	0.00054	0.31	0.78		PHOSPHOTRANSFERASE NUCLEOSIDE DIPHOSPHATE KINASE (E.C.2.7.4.6) COMPLEXED WITH 1NHK 3 5'-CYCLIC ADENOSINE MONOPHOSPHATE 1NHK 4	
482	1npk		250	308	0.00054	0.13	1.00		PHOSPHOTRANSFERASE(PO4 AS ACCEPTOR) NUCLEOSIDE DIPHOSPHATE KINASE (E.C.2.7.4.6) 1NPK 3	
482	1nsq	A	251	308	0.00081	-0.06	0.77		PHOSPHOTRANSFERASE NUCLEOSIDE DIPHOSPHATE KINASE (E.C.2.7.4.6) 1NSQ 3	
482	1nue	A	251	310	0.00027	-0.31	0.09		NUCLEOSIDE DIPHOSPHATE KINASE; 1NUE 4 CHAIN: A, B, C, D,	PHOSPHOTRANSFERASE NUCLEOSIDE TRIPHOSPHATE, NUCLEOSIDE DIPHOSPHATE 1NUE 10

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
489	1cg7	A	75	167	1.1e-29			77.91	NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
489	1cg7	A	93	165	1.1e-29	0.59	1.00		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
489	1ckt	A	8	78	1.1e-24	0.80	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
489	1ckt	A	8	78	1.1e-24			106.80	HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
489	1ezj	A	145	211	2.7e-08	0.35	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
489	1req	A	145	211	2.2e-08	0.28	-0.20		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
489	2trc	P	145	218	2.7e-10	0.13	-0.18		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEK4, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									B, F; 1NUE 5	
483	1avl	A	1	174	0.00081			50.39	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
483	1cnn	A	11	150	2.7e-05	-0.43	0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
484	1b7f	A	48	134	0.00014	0.07	0.13		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
484	1cvj	A	48	134	0.0027	0.44	0.07		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
484	1cvj	B	48	134	0.0027	0.25	0.31		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
484	1cvj	F	48	134	0.0027	0.28	0.03		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
490	1pns		28	108	2.7e-10	0.12	0.98		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
494	1suv	A	10	212	3.4e-41	0.20	1.00		ULP1 PROTEASE; CHAIN: A; UBITQUTIN-LIKE PROTEIN SMT3; CHAIN: B;	HYDROLASE SUMO HYDROLASE, UBIQUITIN-LIKE PROTEASE 1, SMT3 HYDROLASE 2 DESUMOYLATING ENZYME, CYSTEINE PROTEASE, SUMO PROCESSING 3 ENZYME, SMT3 PROCESSING ENZYME, NABH4, THIOHEMIACETAL, 4 COVALENT PROTEASE ADDUCT
499	1dn1	B	179	323	8.1e-09	0.02	-0.14		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
501	1avt	A	31	226	0.00017			61.44	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
501	1cxn	A	40	245	8.1e-07			54.20	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
490	1awe	A	92	134	0.0054	-0.22	0.42		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
490	1awe		47	111	0.00054	-0.04	0.19		SOS1; CHAIN: NULL;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION, SOS, PLECKSTRIN HOMOLOGY (PH) DOMAIN
490	1bc8	C	90	134	0.0054	-0.30	0.28		E74 PROMOTOR DNA; CHAIN: A, B; SAP-1; CHAIN: C;	COMPLEX (DNA-BINDING PROTEIN/DNA) SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A; ETS DOMAIN, DNA-BINDING DOMAIN, WINGED HELIX-TURN-HELIX, 2 CRYSTAL STRUCTURE, DNA-BINDING SPECIFICITY, COMPLEX 3 (DNA-BINDING PROTEIN/DNA) SHEET HEADER CONECT
490	1btk	A	34	107	0.0011	-0.33	0.89		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
490	1dbh	A	35	109	0.00027	-0.07	0.40		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										STRUCTURAL PROTEIN
501	1qsu	A	20	243	2.7e-07			35.43	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
502	1ad0	A	20	225	1.7e-82			101.11	FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
502	1afv	L	21	224	3.4e-78			101.19	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
502	1ay1	L	20	226	1.2e-79	0.19	0.98		TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
502	1b2w	L	20	229	6.8e-87	0.15	0.84		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
502	1b2w	L	21	225	6.8e-87			109.95	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										GENE REGULATION
490	1dux	C	91	134	0.0027	-0.08	0.22		DNA (5'-D(*TP*GP*AP*CP*CP*GP*GP*AP*AP*GP*TP*GP*T) CHAIN: A, D; DNA (5'-D(*AP*CP*AP*CP*TP*TP*CP*CP*GP*GP*TP*CP*A) CHAIN: B, E; ETS-DOMAIN PROTEIN ELK-1; CHAIN: C, F;	TRANSCRIPTION/DNA TRANSFORMING PROTEIN ELK-1, ELK1, MEMBER OF ETS ETS-DOMAIN, DNA-BINDING DOMAIN, WINGED HELIX-TURN-HELIX, 2 CRYSTAL STRUCTURE, DNA-BINDING SPECIFICITY
490	1ctc		90	134	0.0027	-0.47	0.09		MURINE ETS-1 TRANSCRIPTION FACTOR; 1ETC 4 CHAIN: NULL; 1ETC 5	TRANSCRIPTION REGULATION
490	1fao	A	28	106	2.2e-13	0.73	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
490	1fb8	A	28	106	5.4e-13	0.92	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
490	1fgy	A	28	106	5.4e-12	0.91	1.00		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
490	1fli	A	80	135	0.0027	-0.07	0.09		FLI-1; 1FLI 5 CHAIN: A; 1FLI 6 DNA 1FLI 10 CHAIN: B, C; 1FLI 12	COMPLEX (TRANSCRIPTION FACTOR/DNA)
490	1pls		28	106	5.4e-11	0.29	1.00		PHOSPHORYLATION PLECKSTRIN (N-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										INTERFERON, IMMUNE SYSTEM
502	1b6d	A	20	226	1.4e-86	0.11	0.96		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
502	1b6d	A	21	234	1.4e-86			109.72	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
502	1bbj	L	21	233	1.4e-78			102.84	IMMUNOGLOBULIN FAB' FRAGMENT OF MONOCLONAL ANTIBODY B72.3 1BBJ 3 (MURINE/HUMAN CHIMERA) 1BBJ 4	
502	1bd2	D	21	219	8.1e-74			233.42	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
502	1bfo	A	21	235	5.1e-79			105.12	CAMPATH-1G ANTIBODY; CHAIN: A, B, C, D, E, F, G, H;	ANTIBODY ANTIBODY, FAB, CAMPATH-1G, CD52
502	1bj1	L	20	228	1.4e-88	0.03	0.90		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
502	1bj1	L	21	224	1.4e-88			109.40	FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
502	1ce1	L	20	226	6.8e-85	0.27	0.99		CAMPATH-1H:LIGHT CHAIN; CHAIN: L;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	
502	1ce1	L	21	233	6.8e-85			108.57	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
502	1cz8	A	21	225	5.1e-75			105.20	7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
502	1dee	A	20	229	1.2e-89	0.06	0.95		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
502	1dfb	L	21	225	1e-84			107.04	IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
502	1f11	A	20	226	1.7e-79	0.05	1.00		F124 IMMUNOGLOBULIN (KAPPA LIGHT CHAIN); CHAIN: A, C; F124 IMMUNOGLOBULIN (IGG1 HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, ANTIBODY, FAB, HEPATITIS B, PRES2
502	1fig	L	20	225	5.1e-81			103.10	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB FRAGMENT 1FIG 3	
502	1fns	L	20	229	1.7e-85	0.18	0.77		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
	1fvd	A	20	229	1.4e-86	0.08	0.98		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
502	1fvd	A	21	225	1.4e-86			106.39	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
502	1gc1	L	21	233	1.5e-81			108.90	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
502	1gc1	L	23	226	1.5e-81	0.17	1.00		ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
502	1hil	A	20	226	5.1e-81	0.14	0.90		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	
502	1ifh	L	20	226	5.1e-81	0.00	0.81		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WITH PEPTIDE OF 1IFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) 1IFH 4	
502	1igt	A	20	229	3.4e-85	0.14	0.90		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
502	1igt	A	21	225	3.4e-85			102.74	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
502	1kb5	L	21	225	1.7e-83			108.53	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
502	1nsn	L	20	228	3.4e-81	0.10	0.86		IGG FAB (IGG1, KAPPA); 1NSN 4 CHAIN: L, H; 1NSN 5 STAPHYLOCOCCAL NUCLEASE; 1NSN 9 CHAIN: S; 1NSN 10	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) N10 FAB IMMUNOGLOBULIN; 1NSN 7 STAPHYLOCOCCAL NUCLEASE RIBONUCLEATE, 1NSN 11 IMMUNOGLOBULIN, STAPHYLOCOCCAL NUCLEASE 1NSN 25
502	1qrn	D	21	222	2.4e-68			251.37	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
502	1sbn	L	20	229	5.1e-85	0.20	0.98		MONOCLONAL ANTIBODY 3A2; CHAIN: H,	MONOCLONAL ANTIBODY, MONOCLONAL ANTIBODY, FAB-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
503	1bec		23	180	5.4e-51	0.47	1.00		14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
503	1fyt	E	23	180	5.4e-37	0.36	1.00		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DR1, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
505	1btn		153	246	1.1e-11	0.88	0.88		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
505	1dro		153	251	5.4e-15	0.67	0.76		BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	CYTOSKELETON
505	1e0m	A	35	62	0.0014	0.08	0.25		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
505	1f8a	B	35	65	0.00054	0.08	0.07		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	ISOMERASE PIN1; PEPTIDYL-PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
505	1fao	A	136	253	2.7e-11	0.61	0.94		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
505	1fb8	A	136	253	8.1e-11	0.60	0.82		DUAL ADAPTOR OF PHOSPHOTYROSINE AND	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									L;	FRAGMENT, REPRODUCTION
502	1tcr	A	21	227	1.4e-74			181.32	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
502	1vge	L	21	225	1.7e-85			106.15	TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
502	1vgc	L	22	229	1.7e-85	0.05	0.87		TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
502	2sc8	L	20	226	5.1e-81	0.04	0.72		10G 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
502	2fgw	L	20	229	3.4e-89	0.09	0.95		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY H52 (HUH52-OZ FAB) 2FGW 4	
502	2fgw	L	21	225	3.4e-89			111.79	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY H52 (HUH52-OZ FAB) 2FGW 4	
502	3fct	A	22	228	5.1e-81	0.20	0.83		METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
503	1so7	E	22	180	2.7e-49	0.29	1.00		HLA-A 0201; CHAIN: A;	COMPLEX (MHC/VIRAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									3- CHAIN: A;	PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
505	1fgy	A	158	252	8.1e-06	0.74	0.88		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
505	1pls		136	250	2.7e-10	0.18	0.80		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEH)) (NMR, 25 STRUCTURES) 1PLS 5	
505	1pns		130	252	1.9e-14	0.41	0.36		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
505	1qqg	A	138	315	1.9e-12	0.21	0.17		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
507	1ffk	E	11	93	1.7e-19	-0.29	0.64		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L7AE; CHAIN: E;	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL4; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 30S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
503	1so7	E	22	180	2.7e-49			132.96	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
503	1bd2	E	22	180	5.4e-54	0.48	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
503	1bd2	E	22	180	5.4e-54			147.96	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
503	1bec		22	180	5.4e-51			135.25	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B, C, D;	BIOSYNTHESIS
509	1dfo	A	27	500	1.2e-77	0.17	-0.02		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
509	1eg5	A	50	492	1.7e-65	0.30	0.96		AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE PLP-DEPENDENT ENZYMES, IRON-SULFUR-CLUSTER SYNTHESIS, C-S 2 BETA LYASE
509	1cjj	A	27	499	1e-65	0.23	0.31		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE-GLYCINE CONVERSION, PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER
509	1chu	A	41	442	3.4e-47	0.54	0.93		L-CYSTEINE/L-CYSTINE C-S LYASE; CHAIN: A, B;	LYASE FES CLUSTER BIOSYNTHESIS, PYRIDOXAL 5'-PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME-PRODUCT COMPLEX
509	1cgs	A	81	492	3.4e-58	0.41	-0.05		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D, E, F, G, H;	LYASE METHIONINE BIOSYNTHESIS, PYRIDOXAL 5'-PHOSPHATE, GAMMA-2 FAMILY, LYASE
509	2gss	A	45	319	1.4e-10	0.16	0.00		GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'-PHOSPHATE, 2 PYRIDOXAMINE-5'-PHOSPHATE, ASYMMETRIC DIMER
512	1a1h	A	769	876	2.7e-05	-0.16	0.17		QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L10E; CHAIN: P; RIBOSOMAL PROTEIN L13; CHAIN: O; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L15; CHAIN: J; RIBOSOMAL PROTEIN L18; CHAIN: K; RIBOSOMAL PROTEIN L18E; CHAIN: L; RIBOSOMAL PROTEIN L19; CHAIN: M; RIBOSOMAL PROTEIN L21E; CHAIN: N; RIBOSOMAL PROTEIN L22; CHAIN: O; RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V;	HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL13; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
512	1mbn		642	689	0.00085	-0.18	0.46		MYB PROTO-ONCOGENE PROTEIN; IMBE 4	DNA BINDING PROTEIN PROTOONCOGENE PRODUCT IMBE 12
512	1mey	C	792	876	0.00022	0.21	0.72		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
512	1a1h	A	769	864	1.1e-07	-0.01	0.65		QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
512	1idy		639	694	0.0075	-0.02	0.33		MOUSE C-MYB DNA-BINDING DOMAIN REPEAT 3; CHAIN: NULL;	DNA-BINDING PROTEIN PROTOONCOGENE PRODUCT, DNA-BINDING PROTEIN
512	1mbn		642	680	0.0026	-0.36	0.22		MYB PROTO-ONCOGENE PROTEIN; IMBE 4	DNA BINDING PROTEIN PROTOONCOGENE PRODUCT IMBE 12
512	1mse	C	639	694	0.0075	-0.35	0.30		COMPLEX (BINDING PROTEIN/DNA) C-MYB DNA-BINDING DOMAIN COMPLEXED WITH DNA IMSE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IMSE 4 IMSE 84	
512	1ubd	C	771	864	8.1e-06	0.16	0.04		YY1; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E; CHAIN: Z; RIBOSOMAL PROTEIN L6; CHAIN: 1;	
509	1ax4	A	43	320	1.7e-10	0.09	-0.11		TRYPTOPHANASE; CHAIN: A, B, C, D;	TRYPTOPHAN BIOSYNTHESIS TRYPTOPHAN INDOLE-LYASE; TRYPTOPHAN BIOSYNTHESIS, TRYPTOPHAN INDOLE-LYASE, PYRIDOXAL 2 5'-PHOSPHATE, MONOVALENT CATION BINDING SITE
509	1bj4	A	27	499	1.5e-67	0.20	-0.06		SERINE HYDROXYMETHYLTRANSFIRASE; CHAIN: A;	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'-PHOSPHATE
509	1c0n	A	33	488	5.1e-76	0.37	1.00		CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOLD
509	1c7n	A	61	289	1.7e-06	-0.09	0.00		CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE
509	1cjO	A	27	499	3.4e-68	0.25	0.00		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE, 1 CARBON METABOLISM
509	1cl1	A	58	492	3.4e-43	0.25	0.16		CYSTATHIONINE BETA-LYASE; CHAIN: A, B;	METHIONINE BIOSYNTHESIS BETA CYSTATHIONASE; PLP-DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS, C-S BETA 2 LYASE
509	1cs1	A	68	492	1.7e-52	0.33	-0.15		CYSTATHIONINE GAMMA-SYNTHASE;	LYASE CGS; LYASE, LLP-DEPENDENT ENZYMES, METHIONINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(SC/APKS) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
514	1ckl	A	1	300	1.5e-84			285.79	CASEIN KINASE I DELTA; 1CKI 6 CHAIN: A, B; 1CKI 7	PHOSPHOTRANSFERASE PROTEIN KINASE 1CKI 18
514	1ckl	A	3	295	1.5e-84	0.64	1.00		CASEIN KINASE I DELTA; 1CKI 6 CHAIN: A, B; 1CKI 7	PHOSPHOTRANSFERASE PROTEIN KINASE 1CKI 18
514	1cmk	E	2	336	0			75.82	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
514	1csn		1	294	3.4e-78	0.73	1.00		CASEIN KINASE-1; 1CSN 4	PHOSPHOTRANSFERASE
514	1csn		7	291	3.4e-78			293.57	CASEIN KINASE-1; 1CSN 4	PHOSPHOTRANSFERASE
514	1ctp	E	1	325	0			77.16	TRANSFERASE(PHOSPHO TRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
520	1avl	A	69	271	6.8e-06			69.36	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
512	2gli	A	769	864	5.4e-06	0.21	0.39		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
513	1a1h	A	769	876	2.7e-05	-0.16	0.17		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
513	1mbe		642	689	0.00085	-0.18	0.46		MYB PROTO-ONCOGENE PROTEIN; 1MBE 4	DNA BINDING PROTEIN PROTOONCOGENE PRODUCT 1MBE 12
513	1mey	C	792	876	0.00022	0.21	0.72		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
513	1a1h	A	769	864	1.1e-07	-0.01	0.65		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
513	1idy		639	694	0.0075	-0.02	0.33		MOUSE C-MYB DNA-BINDING DOMAIN REPEAT 3; CHAIN: NULL;	DNA-BINDING PROTEIN PROTOONCOGENE PRODUCT, DNA-BINDING PROTEIN
513	1mbe		642	680	0.0026	-0.36	0.22		MYB PROTO-ONCOGENE PROTEIN; 1MBE 4	DNA BINDING PROTEIN PROTOONCOGENE PRODUCT 1MBE 12
513	1mse	C	639	694	0.0075	-0.35	0.30		COMPLEX (BINDING PROTEIN/DNA) C-MYB DNA-BINDING DOMAIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ACTIVATION
520	1qus	A	101	352	5.4e-12			74.38	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
520	1sig		1	299	2.2e-10			78.92	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
526	1chc		12	66	5.4e-11	0.27	0.78		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
526	1fbv	A	16	59	1.7e-09	-0.34	0.03		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
526	1fbv	A	16	71	1.1e-11	-0.19	0.15		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
526	1fre		96	133	5.4e-12	-0.63	0.34		NUCLEAR FACTOR XNF7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-TRANSITION
526	1fre		98	134	0.00068	-0.53	0.53		NUCLEAR FACTOR XNF7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									COMPLEXED WITH DNA 1MSE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1MSE 4 1MSE 84	
513	1ubd	C	771	864	8.1e-06	0.16	0.04		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
513	2gli	A	769	864	5.4e-06	0.21	0.39		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
514	1apm	E	1	336	0			77.95	TRANSFERASE(PHOSPHO TRANSFERASE) SC-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APKS) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139AS) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
514	1apm	E	3	327	0	-0.21	0.13		TRANSFERASE(PHOSPHO TRANSFERASE) SC-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										REPEAT
532	1qav	A	199	254	5.4e-07	-0.33	0.05		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEINOXIDOREDUCTASE BETA-FINGER, HETERODIMER
532	1qlc	A	208	272	5.4e-05	-0.38	0.41		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
532	3pdz	A	208	273	2.4e-05	-0.26	0.84		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
533	1b8q	A	208	251	1.6e-05	-0.43	0.98		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
533	1be9	A	214	251	1.4e-05	-0.55	0.77		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
533	1i16		198	251	1.1e-05	-0.11	0.46		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
533	1kwa	A	203	260	5.4e-07	-0.52	0.59		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
533	1pdr		204	239	1.6e-05	-0.62	0.47		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
533	1qav	A	199	254	5.4e-07	-0.33	0.05		ALPHA-1 SYNTROPHIN (RESIDUES 77-171);	MEMBRANE PROTEINOXIDOREDUCTASE BETA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										TRANSITION
526	1g25	A	12	72	1.4e-13	0.16	0.37		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
526	1g25	A	16	66	5.1e-05	-0.04	0.25		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
526	1rmd		10	103	2.4e-19	-0.04	0.47		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
526	1rmd		3	101	8.5e-13	-0.28	0.23		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
532	1b8q	A	208	251	1.6e-05	-0.43	0.98		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
532	1be9	A	214	251	1.4e-05	-0.55	0.77		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
532	1i16		198	251	1.1e-05	-0.11	0.46		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
532	1kwa	A	203	260	5.4e-07	-0.52	0.59		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										KINASE
532	1pdr		204	239	1.6e-05	-0.62	0.47		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
532	1qav	A	199	254	5.4e-07	-0.33	0.05		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEINOXIDOREDUCTASE BETA-FINGER, HETERODIMER
532	1qlc	A	208	272	5.4e-05	-0.38	0.41		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
532	3pdz	A	208	273	2.4e-05	-0.26	0.84		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
532	1b8q	A	208	251	1.6e-05	-0.43	0.98		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
532	1be9	A	214	251	1.4e-05	-0.55	0.77		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
532	1i16		198	251	1.1e-05	-0.11	0.46		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
532	1kwa	A	203	260	5.4e-07	-0.52	0.59		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
532	1pdr		204	239	1.6e-05	-0.62	0.47		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	FINGER, HETERODIMER
533	1qlc	A	208	272	5.4e-05	-0.38	0.41		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
533	3pdz	A	208	273	2.4e-05	-0.26	0.84		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
533	1b8q	A	208	251	1.6e-05	-0.43	0.98		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
533	1be9	A	214	251	1.4e-05	-0.55	0.77		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
533	1i16		198	251	1.1e-05	-0.11	0.46		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
533	1kwa	A	203	260	5.4e-07	-0.52	0.59		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
533	1pdr		204	239	1.6e-05	-0.62	0.47		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
533	1qav	A	199	254	5.4e-07	-0.33	0.05		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEINOXIDOREDUCTASE BETA-FINGER, HETERODIMER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
542	1abr	B	559	636	5.1e-13	-0.43	0.27		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS 1ABR 3	
542	1qgq	A	191	431	1.4e-21	0.13	0.58		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN CHAIN: A;	TRANSFERASE GLYCOSYLTRANSFERASE
542	1xyf	A	496	629	1.7e-30	0.30	0.69		ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
542	1xyf	A	546	636	1e-17	0.04	0.70		ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
543	1c4o	A	559	681	5.4e-11	0.25	0.65		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
543	1d2m	A	559	681	2.7e-10	0.23	0.54		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
543	1d9x	A	536	683	2.4e-18	0.61	1.00		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
543	1fuk	A	544	682	1.1e-11	0.71	0.60		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
543	1fuu	B	555	652	1.6e-11	0.36	0.62		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
546	1e0g	A	65	107	8.5e-08	-0.72	0.04		MEMBRANE-BOUND LYTIC MUREIN	HYDROLASE MLTD, MUREIN HYDROLASE D, REGULATORY

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
533	1qlc	A	208	272	5.4e-05	-0.38	0.41		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
533	3pdz	A	208	273	2.4e-05	-0.26	0.84		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
538	1c4z	A	234	583	0	0.33	1.00		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
538	1c4z	A	234	586	0			227.88	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
541	1a7i		100	159	1.4e-15	0.69	0.94		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
541	1a7i		163	218	1.9e-13	-0.03	0.83		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
541	1a7i		39	94	5.4e-14	0.40	0.93		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
541	1b8t	A	162	281	3.4e-13	0.01	0.84		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TRANSGLYCOSYLASE D; CHAIN: A;	PROTEIN DNIR; CELL WALL, HYDROLASE, GLYCOSIDASE, LIPOPROTEIN, 2 OUTER MEMBRANE, MULTIGENE FAMILY
550	1a1b	A	270	351	1.4e-27	-0.04	0.86		QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
550	1mey	C	101	182	8.5e-44	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	157	238	3.4e-47	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	185	266	8.5e-48	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	213	293	1.7e-46	0.61	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	241	351	1.1e-39	0.02	0.69		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
541	1b8t	A	33	236	5.1e-14			96.09	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
541	1ctl		38	94	5.4e-16	0.19	1.00		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
541	1ctl		99	155	5.4e-13	0.30	0.82		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
541	1cxx	A	160	215	2.7e-13	0.44	0.71		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
541	1cxx	A	38	94	1.6e-15	0.74	1.00		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
541	1cxx	A	99	157	1.4e-14	0.10	0.98		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
541	1ext	A	104	270	6.8e-07			59.59	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
541	1lm1		101	170	1.1e-15	0.12	0.41		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
541	1lm1		163	230	5.4e-21	0.05	0.64		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
541	1lm1		41	111	5.4e-17	0.27	0.27		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
541	1klo		72	241	0.00027			62.78	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
541	1ncf	A	22	166	3.4e-07			52.60	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	158	304	3.4e-34	0.18	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	186	332	1.7e-34	-0.21	0.70		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	383	529	1e-37	0.05	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	411	549	3.4e-36	0.21	0.84		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	93	219	1.7e-30	-0.00	0.89		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1ubd	C	104	210	6.8e-32	0.17	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	269	351	1.7e-46	-0.06	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	298	379	1.5e-49	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	326	407	1.4e-50	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	354	435	8.5e-51	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	382	463	1e-50	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	410	491	1.7e-50	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	438	519	1e-50	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DNA; CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	111	210	8.1e-45	-0.08	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	134	238	2.7e-54	-0.21	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	155	266	5.4e-56	0.27	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	183	292	5.4e-52	-0.20	0.75		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	221	323	6.8e-31	0.11	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	438	520	1e-50			107.02	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	466	547	5.1e-50	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	494	352	8.5e-35	0.20	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1mey	C	85	154	1e-33	-0.44	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
550	1tf6	A	102	247	5.1e-35	-0.13	0.59		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
550	1tf6	A	127	295	3.4e-36			107.82	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
550	2gli	A	157	297	2.2e-67	0.40	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	185	353	1.6e-65	0.10	0.45		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	249	378	8.5e-33	0.18	0.58		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	298	437	2.7e-68	0.39	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	382	549	8.1e-73	-0.09	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	390	518	6.8e-35	0.17	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
553	1cmz	A	73	200	1.4e-51	0.47	1.00		GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
553	1cmz	A	73	200	1.4e-51			172.06	GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										PROTEIN, SIGNALING PROTEIN 2 REGULATION
553	1cmz	A	73	200	3.4e-47	0.47	1.00		GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
555	1sus		17	277	8.5e-61			92.44	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SEC14P; CHAIN: NULL;	PHOSPHOLIPID-BINDING PROTEIN PHOSPHOLIPID-BINDING PROTEIN, PERIPHERAL GOLGI MEMBRANE 2 PROTEIN, PHOSPHOLIPID EXCHANGE, GOLGI-DERIVED SECRETORY 3 VESICLE BIOGENESIS
555	1sus		43	274	8.5e-61	0.22	1.00		PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SEC14P; CHAIN: NULL;	PHOSPHOLIPID-BINDING PROTEIN PHOSPHOLIPID-BINDING PROTEIN, PERIPHERAL GOLGI MEMBRANE 2 PROTEIN, PHOSPHOLIPID EXCHANGE, GOLGI-DERIVED SECRETORY 3 VESICLE BIOGENESIS
557	1e07	A	444	534	1.7e-19	0.87	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
557	1d2e	A	56	424	1.4e-83	-0.44	0.03		ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
557	1ega	A	61	263	0.001	-0.24	0.09		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA-BINDING, RAS-LIKE, HYDROLASE
557	1eh2		443	536	1.7e-39			94.67	EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	239	380	5.4e-50	-0.31	0.17		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	277	379	1.4e-33	-0.16	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	296	407	1.1e-51	0.23	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	381	491	1.4e-58	0.14	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	410	520	1.4e-58			90.51	YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	436	547	8.1e-56	0.04	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	1ubd	C	446	547	6.8e-35	0.12	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
550	2adr		242	297	8.5e-16	0.08	0.65		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
550	2gli	A	111	212	2.7e-43	0.09	0.90		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	130	268	1.1e-70	0.37	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
550	2gli	A	157	296	1.1e-70			100.42	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V; RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E; CHAIN: Z; RIBOSOMAL PROTEIN L6; CHAIN: 1;	
559	1ffk	Z	4	93	2.7e-45	-0.53	0.03		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L7AE; CHAIN: E; RIBOSOMAL PROTEIN L10E; CHAIN: F; RIBOSOMAL PROTEIN L13; CHAIN: G; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L15; CHAIN: J; RIBOSOMAL PROTEIN	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 30S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
557	1eh2		444	536	1.7e-39	1.11	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
557	1etu		52	284	1e-52	-0.02	0.11		TRANSPORT AND PROTECTION PROTEIN ELONGATION FACTOR TU (DOMAIN I) - *GUANOSINE DIPHOSPHATE 1ETU 4 COMPLEX 1ETU 5	
557	1g7s	A	59	331	6.8e-13	-0.05	0.05		TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;	TRANSLATION TRANSLATIONAL GTPASE
557	1rro		428	506	0.0011	0.06	0.13		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	
557	2cfg	A	56	222	1.4e-13	-0.40	0.10		ELONGATION FACTOR G; CHAIN: A; ELONGATION FACTOR G DOMAIN 3; CHAIN: B;	PROTEIN BINDING EF-G; EF-G ELONGATION FACTOR, TRANSLOCASE, RIBOSOME, ELONGATION, 2 TRANSLATION, PROTEIN SYNT FACTOR, GTPASE, GTP BINDING, 3 GUANOSINE NUCLEOTIDE BINDING, PROTEIN BINDING
559	1ffk	Z	2	92	5.1e-30	-0.34	0.18		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 30S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									L18; CHAIN: K; RIBOSOMAL PROTEIN L18E; CHAIN: L; RIBOSOMAL PROTEIN L19; CHAIN: M; RIBOSOMAL PROTEIN L21E; CHAIN: N; RIBOSOMAL PROTEIN L22; CHAIN: O; RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN L31E; CHAIN: U; RIBOSOMAL PROTEIN L32E; CHAIN: V; RIBOSOMAL PROTEIN L37AE; CHAIN: W; RIBOSOMAL PROTEIN L37E; CHAIN: X; RIBOSOMAL PROTEIN L39E; CHAIN: Y; RIBOSOMAL PROTEIN L44E; CHAIN: Z; RIBOSOMAL PROTEIN L6; CHAIN: 1;	HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L7AE; CHAIN: E; RIBOSOMAL PROTEIN L10E; CHAIN: F; RIBOSOMAL PROTEIN L13; CHAIN: G; RIBOSOMAL PROTEIN L14; CHAIN: H; RIBOSOMAL PROTEIN L15E; CHAIN: I; RIBOSOMAL PROTEIN L15; CHAIN: J; RIBOSOMAL PROTEIN L18; CHAIN: K; RIBOSOMAL PROTEIN L18E; CHAIN: L; RIBOSOMAL PROTEIN L19; CHAIN: M; RIBOSOMAL PROTEIN L21E; CHAIN: N; RIBOSOMAL PROTEIN L22; CHAIN: O; RIBOSOMAL PROTEIN L23; CHAIN: P; RIBOSOMAL PROTEIN L24; CHAIN: Q; RIBOSOMAL PROTEIN L24E; CHAIN: R; RIBOSOMAL PROTEIN L29; CHAIN: S; RIBOSOMAL PROTEIN L30; CHAIN: T; RIBOSOMAL PROTEIN	PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10 RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
562	1tcr	A	24	189	1.4e-57			118.15	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
562	1vge	L	26	180	1.7e-66	0.22	0.99		TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
562	2fgw	L	23	180	5.1e-68	-0.09	0.90		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
563	1icf	I	83	147	1.4e-24	0.47	1.00		CATHEPSIN L: HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L: LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
563	1icf	I	83	147	2.7e-26	0.47	1.00		CATHEPSIN L: HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L: LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
563	1iic	A	7	81	1.1e-41	-0.31	1.00		HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN; CHAIN: A, B, C;	MAJOR HISTOCOMPATIBILITY COMPLEX HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA MAJOR HISTOCOMPATIBILITY COMPLEX, ANTIGEN PROCESSING, 2 OLIGOMERIZATION, CHAPERONIN
563	1iic	A	7	81	1.1e-41			136.01	HLA-DR ANTIGENS	MAJOR HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
561	1fyv	A	73	168	5.4e-15	-0.13	0.31		TOLL-LIKE RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN BETA-ALPHA-BETA POLD PARALLEL BETA SHEET
561	1fyx	A	86	213	1.7e-20	0.09	0.17		TOLL-LIKE RECEPTOR 2; CHAIN: A;	SIGNALING PROTEIN BETA-ALPHA-BETA FOLD
562	1b2w	L	23	180	5.1e-67	0.10	0.88		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
562	1b6d	A	23	180	1e-66	0.20	0.99		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
562	1bd2	D	24	189	3.4e-57			130.55	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
562	1bj1	L	23	180	1.7e-68	0.24	0.92		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
562	1bz7	A	23	189	1e-59			57.72	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
562	1dee	A	23	180	3.4e-69	-0.12	0.93		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B,	IMMUNE SYSTEM FAB-IBF COMPLEX CRYSTAL STRUCTURE 2.7A

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ASSOCIATED INVARIANT CHAIN; CHAIN: A, B, C;	COMPLEX HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA MAJOR HISTOCOMPATIBILITY COMPLEX, ANTIGEN PROCESSING, 2 OLIGOMERIZATION, CHAPERONIN
563	1iic	A	7	81	1.4e-24	-0.31	1.00		HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN; CHAIN: A, B, C;	MAJOR HISTOCOMPATIBILITY COMPLEX HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA MAJOR HISTOCOMPATIBILITY COMPLEX, ANTIGEN PROCESSING, 2 OLIGOMERIZATION, CHAPERONIN
568	1a1h	A	427	512	1e-22	-0.45	0.11		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
568	1a1h	A	488	570	1.2e-21	0.10	-0.09		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
568	1a1h	A	544	604	1.7e-17	0.30	-0.07		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
568	1ard		544	574	0.0001	0.06	0.10		TRANSCRIPTION REGULATION YEAST	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
562	1fvd	A	23	180	6.8e-66	-0.05	0.76		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
562	1mcp	L	23	183	1.7e-66	-0.13	0.74		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MC/PC603) 1MCP 4	
562	1nfd	A	24	189	5.1e-52			115.80	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
562	1qlr	A	27	180	3.4e-67	-0.18	0.98		IGM KAPPA CHAIN V-III (KAU COLD AGGLUTININ); CHAIN: A, C; IGM FAB REGION IV-J(H4)-C (KAU COLD AGGLUTININ); CHAIN: B, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, AUTOANTIBODY, COLD AGGLUTININ, HUMAN IGM 2 FAB FRAGMENT
562	1qrn	D	24	189	3.4e-53			126.38	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
562	1sbs	L	23	183	3.4e-66	-0.09	0.46		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CELL CYCLE CONTROL FACTOR
569	1g41	A	476	739	1.4e-22	0.05	0.88		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
569	1g41	A	477	730	1e-15	-0.12	0.23		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
569	1shk	A	511	537	0.0014	-0.50	0.21		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
570	1a17		50	170	8.1e-05	0.38	0.48		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
570	1elr	A	110	192	0.00054	0.28	0.10		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
570	1elw	A	162	233	1.6e-05	-0.06	0.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
570	1elw	A	4	143	0.0027	0.07	0.72		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
570	1fch	A	6	150	5.4e-05	0.07	0.45		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
574	1byx	A	143	288	8.1e-16	-0.02	0.57		ENDONUCLEASE; CHAIN: A;	ENDONUCLEASE ENDONUCLEASE, PHOSPHODIESTERASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TRANSCRIPTION FACTOR ADR1 (RESIDUES 102 - 130) 1ARD 3 (AMINO TERMINAL ZINC FINGER DOMAIN) (NMR, 10 STRUCTURES) 1ARD 4 (ADR1B) 1ARD 5	
568	1bbi		543	570	0.00034	-0.09	0.66		CRE-BP1; CHAIN: NULL;	DNA-BINDING REGULATORY PROTEIN ATF-2; CRE BINDING PROTEIN, ATF-2, TRANSCRIPTIONAL ACTIVATION 2 DOMAIN, ZN FINGER
568	1mey	C	543	604	6.8e-25	0.16	-0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
568	1mey	G	309	339	5.1e-11	0.11	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
568	1mey	G	541	570	1.2e-11	-0.21	0.11		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
568	1pax		544	572	0.00085	-0.37	0.51		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADR1 (RESIDUES 130 - 159) 1PAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH 1PAA 4 PRO 131	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
575	1aox	A	166	363	3.4e-36	1.09	1.00		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
575	1aox	A	166	366	3.4e-36			191.82	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
575	1auq		156	370	3.4e-40	0.21	0.99		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
575	1ck4	A	169	361	1.9e-61	1.20	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
575	1ck4	A	171	359	1.7e-35	1.12	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
575	1fna	A	166	367	1e-37	0.47	1.00		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
575	1qc5	A	168	359	5.4e-45	1.16	1.00		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
575	1qc5	A	171	359	6.8e-36	1.16	1.00		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
583	1a1h	A	201	283	5.4e-37	0.27	1.00		QSSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
583	1a1h	A	201	283	5.4e-37			90.89	QSSR ZINC FINGER	COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 1PAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) 1PAA 6	
568	1sp2		544	574	5.1e-10	0.07	0.80		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
568	1tf3	A	544	605	6.8e-11	0.18	-0.18		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
568	1zfd		543	570	3.4e-06	0.19	0.29		SWI5; CHAIN: NULL;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
568	2adr		544	576	8.5e-06	0.26	0.03		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
569	1d2n	A	489	640	1.7e-13	0.29	0.82		N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
569	1e94	E	477	598	3.4e-12	-0.51	0.05		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
569	1fnn	A	490	732	1.9e-14	0.01	-0.05		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITATION 2 FACTOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	G	254	281	1.6e-10	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1tf3	A	229	305	1.2e-13	-0.07	0.11		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
583	1tf6	A	145	316	6.8e-36	0.04	0.82		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
583	1tf6	A	43	178	1.5e-34	0.41	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
583	1tf6	A	60	225	1e-38			116.35	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
583	1tf6	A	61	206	1.2e-38	0.49	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
583	1a1h	A	229	296	2.7e-24	-0.05	0.93		QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
583	1a1h	A	229	309	5.1e-23	0.10	0.88		QSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
583	1b8r	A	112	315	5.4e-13			55.06	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
583	1mey	C	116	197	3.4e-51	0.70	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	116	198	3.4e-51			108.46	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	144	225	6.8e-51	0.58	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
583	1ubd	C	114	225	5.4e-47	0.60	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	152	253	3.4e-35	0.38	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	170	281	2.7e-46	0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	174	282	2.7e-46			96.41	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	198	296	5.4e-35	0.19	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										(ZINC FINGER/DNA)
583	1mey	C	172	253	1.4e-50	0.73	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	200	274	3.4e-46	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	228	309	1.4e-40	-0.01	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	256	317	1e-25	-0.33	0.41		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	44	113	1.2e-39	0.31	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	60	141	1.4e-50	0.77	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
583	1mey	C	88	169	6.8e-51	0.64	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
583	1gp2	G	30	83	6.8e-23	-0.81	0.60		G PROTEIN GI ALPHA 1; CHAIN: A; G PROTEIN GI BETA 1; CHAIN: B; G PROTEIN GI GAMMA 2; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) SIGNAL TRANSDUCTION PROTEIN, GTPASE, WD40, RAS-LIKE, 2 COMPLEX (GTP-BINDING/TRANSDUCER)
585	1gp2	G	30	83	6.8e-23			57.14	G PROTEIN GI ALPHA 1; CHAIN: A; G PROTEIN GI BETA 1; CHAIN: B; G PROTEIN GI GAMMA 2; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) SIGNAL TRANSDUCTION PROTEIN, GTPASE, WD40, RAS-LIKE, 2 COMPLEX (GTP-BINDING/TRANSDUCER)
586	1d2h	A	78	196	1.4e-18	0.49	0.35		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
586	1dus	A	79	197	1.7e-07	-0.11	0.00		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
586	1ej0	A	79	199	0.00017	0.09	0.16		FTSJ; CHAIN: A;	TRANSFERASE FTSJ METHYLTRANSFERASE; FTSJ, METHYLTRANSFERASE, ADOMET, ADENOSYL METHIONINE, HEAT 2 SHOCK PROTEINS, 23S RIBOSOMAL RNA
586	1vid		57	195	8.1e-09	0.28	0.04		CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
586	1xva	A	78	196	1.4e-18	0.32	0.24		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE: GLYCINE METHYLTRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	208	309	1.7e-27	-0.21	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	44	141	8.5e-32	0.44	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	65	169	1.1e-47	0.37	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	1ubd	C	68	169	1.2e-34	0.48	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
583	2adr		257	309	1.7e-08	-0.43	0.01		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
587	1chc		122	179	5.4e-05	-0.16	0.01		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
587	1igr	A	53	169	1.2e-05	-0.22	0.04		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
591	1aj4		10	168	6.8e-45	0.58	0.92		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
591	1aj4		1	170	6.8e-45			69.25	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
591	1akh		14	89	1.7e-29	0.41	0.65		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
591	1aui	B	14	175	1.4e-40	0.58	0.83		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
591	1aui	B	9	179	1.4e-40			65.74	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
591	1svs	A	18	91	3.4e-25	0.67	0.99		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
591	1bjf	A	5	185	3.4e-38			64.29	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
591	1bkj		18	93	5.1e-26	0.50	0.69		N-TROPONIN C; CHAIN:	CALCIUM-BINDING PROTEIN SNTNC;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
583	2gli	A	116	281	2.4e-58	0.40	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	124	252	5.1e-35	0.48	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	152	275	5.1e-32	0.55	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	180	308	6.8e-27	0.38	0.29		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	60	199	1.9e-62			104.54	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	61	199	1.9e-62	0.53	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	68	196	6.8e-34	0.42	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
583	2gli	A	88	227	2.4e-62	0.64	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tcf		9	168	1.2e-47			77.47	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tnx		18	166	5.1e-46	0.50	1.00		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
591	1tnx		9	166	5.1e-46			69.47	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
591	1top		18	168	6.8e-49	0.89	1.00		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1top		2	86	5.1e-24	0.56	0.77		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1top		6	170	6.8e-49			78.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1trc	A	93	167	1.4e-27	0.36	1.00		CALCIUM BINDING PROTEIN CALMODULIN (/TR=>C$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
591	1tcf		18	91	3.4e-25	1.19	1.00		MUSCLE PROTEIN TROPONIN C (TR1C	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
591	1cdm	A	18	167	3.4e-56	0.77	1.00		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
591	1cdm	A	18	167	3.4e-56			65.81	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
591	1cll		18	167	8.5e-61	0.82	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cll		18	168	8.5e-61			75.45	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cll		2	86	1.2e-26	0.74	0.98		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cll		90	184	1.7e-24	0.37	0.46		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cmf		89	169	5.1e-28	0.07	0.84		CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
591	1wrk	A	15	169	1e-59	0.75	1.00		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	1wrk	A	16	169	1e-59			75.17	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	1wrk	A	2	89	1.4e-25	0.15	0.99		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	1wrk	A	87	184	3.4e-23	0.29	0.63		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	3ctn		91	168	1.2e-19	0.22	0.59		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
591	1aj4		12	157	1e-40	0.85	0.98		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
591	1aj4		1	159	1e-40			58.42	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
591	1ak8		14	89	3.4e-30	0.41	0.65		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
591	1evs	A	18	91	1.4e-25	0.67	0.99		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
591	1dtl	A	16	168	8.5e-43	0.71	1.00		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
591	1cxr	A	16	168	5.1e-59	0.57	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
591	1cxr	A	2	86	3.4e-25	0.51	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
591	1cxr	A	88	184	3.4e-23	0.59	0.89		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
591	1f71	A	95	169	3.4e-27	0.58	1.00		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
591	1fi5	A	83	168	6.8e-20	-0.10	0.15		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
591	1iku		1	186	3.4e-29			56.95	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
591	1tcf		18	168	1.2e-47	0.75	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tcf		2	86	5.1e-24	0.45	0.63		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tcf		90	184	8.5e-19	0.32	0.42		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TROPONIN C (TR1C FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
591	1wrk	A	15	157	8.3e-56	0.71	0.98		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	1wrk	A	17	159	8.3e-56			69.15	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	1wrk	A	1	89	1.7e-24	0.30	0.70		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
591	2myn	B	20	145	1.7e-24	-0.16	0.34		MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
592	1aj4		10	168	6.8e-45	0.58	0.92		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
592	1aj4		1	170	6.8e-45			69.25	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
592	1ak8		14	89	1.7e-29	0.41	0.63		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TR1C-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
592	1aui	B	14	175	1.4e-40	0.58	0.83		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CONTRACTION, CALCIUM-ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
591	1blq		18	93	5.1e-26	0.50	0.69		N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
591	1br1	B	19	159	1.2e-33	0.73	0.99		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
591	1cdm	A	18	157	5.1e-54	0.72	1.00		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
591	1cdm	A	19	157	5.1e-54			60.34	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
591	1cll		18	157	1e-57	0.75	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cll		19	158	1e-57			71.03	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
591	1cll		1	86	6.8e-26	0.44	0.90		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
592	1aui	B	9	179	1.4e-40			65.74	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
592	1avs	A	18	91	3.4e-25	0.67	0.99		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
592	1bjf	A	5	185	3.4e-38			64.29	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
592	1blq		18	93	5.1e-26	0.50	0.69		N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
592	1cdm	A	18	167	3.4e-56	0.77	1.00		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
592	1cdm	A	18	167	3.4e-56			65.81	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
592	1cll		18	167	8.5e-61	0.82	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
591	1dtl	A	12	157	1.4e-40	0.69	1.00		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
591	1exr	A	18	158	1.7e-55	0.50	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
591	1exr	A	1	86	3.4e-23	0.53	0.53		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
591	1tcf		12	158	1.7e-44			68.07	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tcf		18	156	1.7e-44	0.28	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
591	1tnx		12	156	3.4e-43			63.93	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
591	1tnx		18	156	3.4e-43	0.51	0.94		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
591	1top		18	156	1.7e-45	0.68	1.00		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1top		1	86	3.4e-23	0.48	0.25		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1top		6	159	1.7e-45			69.75	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
591	1trf		18	91	1.4e-25	1.19	1.00		MUSCLE PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
592	1cll		18	168	8.5e-61			75.45	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1cll		2	86	1.2e-26	0.74	0.98		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1cll		90	184	1.7e-24	0.37	0.46		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1cmf		89	169	5.1e-28	0.07	0.84		CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
592	1dkl	A	16	168	8.5e-43	0.71	1.00		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
592	1exr	A	16	168	5.1e-59	0.57	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
592	1exr	A	2	86	3.4e-25	0.51	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
592	1exr	A	88	184	3.4e-23	0.59	0.89		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
592	1f71	A	95	169	3.4e-27	0.58	1.00		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
592	1f15	A	83	168	6.8e-20	-0.10	0.15		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
592	1iku		1	186	3.4e-29			56.95	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
592	1tcf		18	168	1.2e-47	0.75	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
592	1top		6	170	6.8e-49			78.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 2	
592	1trc	A	93	167	1.4e-27	0.36	1.00		CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=CS FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
592	1trf		18	91	3.4e-25	1.19	1.00		MUSCLE PROTEIN TROPONIN C (TR1C FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
592	1wrk	A	15	169	1e-59	0.75	1.00		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	1wrk	A	16	169	1e-59			75.17	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	1wrk	A	2	89	1.4e-25	0.15	0.99		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	1wrk	A	87	184	3.4e-23	0.29	0.63		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	3ctn		91	168	1.2e-19	0.22	0.59		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tcf		2	86	5.1e-24	0.45	0.63		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tcf		90	184	8.5e-19	0.32	0.42		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tcf		9	168	1.2e-47			77.47	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tnx		18	166	5.1e-46	0.50	1.00		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
592	1tnx		9	166	5.1e-46			69.47	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
592	1top		18	168	6.8e-49	0.89	1.00		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 2	
592	1top		2	86	5.1e-24	0.56	0.77		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
592	1aj4		12	157	1e-40	0.85	0.98		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
592	1aj4		1	159	1e-40			58.42	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
592	1ak8		14	89	3.4e-30	0.41	0.65		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TR1C-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
592	1avs	A	18	91	1.4e-25	0.67	0.99		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
592	1bkj		18	93	5.1e-26	0.50	0.69		N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
592	1br1	B	19	159	1.2e-33	0.73	0.99		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
592	1cdm	A	18	157	5.1e-54	0.72	1.00		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
592	1cdm	A	19	157	5.1e-54			60.24	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SL770; CHAIN: A;	
594	1roq	A	24	114	2.7e-05	0.24	0.31		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
595	1ebd	A	31	83	0.00014	0.98	0.07		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
595	1klo		11	83	0.00016	0.91	0.21		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
600	1f2u	A	51	186	1e-26	-0.08	0.46		RAD50 ABC-ATPASE; CHAIN: A, C; RAD50 ABC-ATPASE; CHAIN: B, D;	REPLICATION DNA DOUBLE-STRAND BREAK REPAIR, ABC-ATPASE
604	1aoe		371	481	5.1e-26	0.72	0.47		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN-BINDING PROTEIN, CALCIUM-BINDING, PHOSPHORYLATION
604	1bkd	A	375	480	1e-35	0.79	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
604	1bkd	A	377	483	1e-35			74.00	UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
604	1bkr	A	378	486	1.5e-45			81.12	SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
604	1bkr	A	379	486	1.5e-43	0.95	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
604	1cii		53	260	5.4e-11	0.17	-0.20		COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
592	1cll		18	157	1e-57	0.75	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1cll		19	158	1e-57			71.03	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1cll		1	86	6.8e-26	0.44	0.90		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
592	1dtl	A	12	157	1.4e-40	0.69	1.00		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
592	1cxr	A	18	158	1.7e-55	0.50	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
592	1cxr	A	1	86	3.4e-23	0.53	0.53		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
592	1mcf		12	158	1.7e-44			68.07	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tcf		18	156	1.7e-44	0.28	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
592	1tnx		12	156	3.4e-43			63.93	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
604	1dxs	A	373	490	1.7e-37	0.58	1.00		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-BINDING, UTROPHIN
604	1ex3	A	109	239	1.6e-08	0.20	-0.17		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
604	1ex3	A	77	192	5.4e-09	0.12	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
604	1ex3	A	91	212	1.1e-08	0.31	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
604	1qag	A	373	485	1.2e-36	0.70	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
604	1qu2	A	88	260	1.1e-09	0.11	-0.20		ISOLEUCYL-TRNA SYNTHETASE; CHAIN: A; ISOLEUCYL-TRNA; CHAIN: T;	LIGASE/RNA ISOLEUCINE--TRNA LIGASE, ILERS; PROTEIN-RNA COMPLEX, METAL IONS, EDITING TRNA SYNTHETASE, 2 DOUBLE-SIEVE
604	1qu1	A	63	259	5.4e-13	0.11	-0.19		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
604	1req	A	1	261	2.7e-21	0.17	-0.18		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
604	2trc	P	167	262	1.9e-09	0.18	-0.19		TRANSDUCIN; CHAIN: B,	COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
592	1ttx		18	156	3.4e-43	0.51	0.94		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
592	1top		18	156	1.7e-45	0.68	1.00		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
592	1top		1	86	3.4e-23	0.48	0.25		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
592	1top		6	159	1.7e-45			69.75	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
592	1trf		18	91	1.4e-25	1.19	1.00		MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
592	1vrk	A	15	157	8.5e-56	0.71	0.98		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	1vrk	A	17	159	8.5e-56			69.15	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	1vrk	A	1	89	1.7e-24	0.30	0.70		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
592	2mys	B	20	145	1.7e-24	-0.16	0.34		MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
594	1qsa	A	24	114	0.0019	-0.04	0.01		SOLUBLE LYTIC TRANSGLYCOSYLASE	TRANSFERASE ALPHA-SUPERHELIX, TRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
629	1a0l	A	24	250	1.4e-73			144.00	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
629	1an5	A	23	250	3.4e-89			197.00	GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE PRORENIN CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION
629	1an5	A	24	250	3.4e-89	1.00	1.00		GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE PRORENIN CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION
629	1aut	C	23	249	3.4e-81			138.35	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
629	1azz	A	24	250	3.4e-63			144.12	COLLAGENASE; CHAIN: A, B; ECOTIN; CHAIN: C, D;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; COMPLEX (SERINE PROTEASE/INHIBITOR), SERINE PROTEASE, 2 INHIBITOR, COMPLEX, PROTEASE-SUBSTRATE INTERACTIONS, 3 COLLAGEN
629	1bio		24	249	2.2e-83			157.25	COMPLEMENT FACTOR D; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, HYDROLASE, COMPLEMENT, FACTOR D, CATALYTIC 2 TRIAD, SELF-REGULATION
629	1bqy	A	24	250	5.1e-79			180.19	PLASMINOGEN ACTIVATOR; CHAIN: A, B;	BLOOD CLOTTING TSV-PA; FIBRINOLYSIS, PLASMINOGEN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									G; PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
604	2trc	P	79	239	8.1e-11	0.12	-0.20		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
612	2plc		10	311	6.8e-67	0.10	0.99		PHOSPHATIDYLINOSITOL -SPECIFIC PHOSPHOLIPASE C; CHAIN: NULL;	HYDROLASE PI-PLC; HYDROLASE, PHOSPHOLIPID DEGRADATION, VIRULENCE FACTOR OF 2 HUMAN PATHOGEN
612	2plc		10	312	6.8e-67			86.97	PHOSPHATIDYLINOSITOL -SPECIFIC PHOSPHOLIPASE C; CHAIN: NULL;	HYDROLASE PI-PLC; HYDROLASE, PHOSPHOLIPID DEGRADATION, VIRULENCE FACTOR OF 2 HUMAN PATHOGEN
612	2ptd		4	301	3.4e-34	0.09	0.71		PHOSPHATIDYLINOSITOL -SPECIFIC PHOSPHOLIPASE C; CHAIN: NULL;	HYDROLASE PI-PLC; HYDROLASE, PHOSPHORIC DIESTER, LIPID DEGRADATION, 2 PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C
612	2ptd		4	314	3.4e-34			74.76	PHOSPHATIDYLINOSITOL -SPECIFIC PHOSPHOLIPASE C;	HYDROLASE PI-PLC; HYDROLASE, PHOSPHORIC DIESTER, LIPID DEGRADATION, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLU-GLY-ARG-CHLOROMETHYLKETONE INHIBITOR; CHAIN: E, F;	ACTIVATOR, SERINE PROTEINASE, 2 SNAKE VENOM, COMPLEX (HYDROLASE/INHIBITOR), BLOOD CLOTTING
629	1dpo		24	250	1.2e-89			197.58	TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
629	1ekb	B	24	249	2.7e-80			145.55	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR
629	1elt		23	248	1e-67			140.39	ELASTASE; 1ELT 4 CHAIN: NULL; 1ELT 5	SERINE PROTEINASE
629	1fcy	A	24	250	8.5e-80			179.71	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
629	1mct	A	23	249	6.8e-95	0.95	1.00		COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
629	1mct	A	24	250	6.8e-95			211.99	COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: NULL;	PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C
617	1cgt		144	339	2.7e-14	0.37	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLYCOSYLTRANSFERASE (E.C.2.4.1.19) 1CGT 3	
617	1cwv	A	98	349	1.4e-31	0.02	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
617	1pzm	A	75	215	2.7e-14	-0.00	-0.19		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
622	1qus	A	42	201	2.2e-13	0.05	0.09		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
627	1a02	J	176	201	0.0081	-0.15	0.58		NFAT; CHAIN: N; C-FOS; CHAIN: P; C-JUN; CHAIN: J; DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION/NUCLEAR/NUCLEAR) NF-AT; TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, NFAT, NF-AT, 2 AP-1, FOS-JUN, QUATERNARY PROTEIN-DNA COMPLEX, CRYSTAL 3 STRUCTURE, TRANSCRIPTION SYNERGY, COMBINATORIAL GENE 4 REGULATION, COMPLEX (TRANSCRIPTION/NUCLEAR/NUCLEAR)
629	1a0j	A	23	250	1.7e-93	1.04	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
629	1a0j	A	24	250	1.7e-93			210.95	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
629	2tbs		24	250	8.5e-91			195.28	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
629	5ptp		23	250	1.7e-91	1.02	1.00		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
629	5ptp		24	250	1.7e-91			202.83	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
632	1a3l	L	21	170	1.7e-78			157.53	IMMUNOGLOBULIN FAB 13G5; CHAIN: L, H;	IMMUNOGLOBULIN DIELS-ALDER, DISFAVORED REACTION, CATALYTIC ANTIBODY, 2 IMMUNOGLOBULIN
632	1a3r	L	21	169	1.7e-90	0.53	1.00		IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPITOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
632	1a3r	L	21	170	1.7e-90			151.40	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPITOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
632	1e4j	L	21	170	1.4e-85			176.88	IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
632	1ed9	L	21	170	1.7e-88			160.46	FAB FRAGMENT CTM01;	IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
629	1npm	A	24	249	2.7e-88			235.42	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
629	1qrz	A	6	250	8.1e-79			132.25	PLASMINOGEN; CHAIN: A, B, C, D;	HYDROLASE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOGEN, CHYMOTRYPSIN 2 FAMILY, HYDROLASE
629	1sgf	A	32	250	8.1e-77			158.03	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
629	1sgf	G	24	250	5.4e-91	0.93	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
629	1sgf	G	24	250	5.4e-91			203.29	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
629	1stw	B	23	249	6.8e-89	0.92	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
629	1stw	B	24	250	6.8e-89			195.91	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L, H, A, B;	IMMUNOGLOBULIN, FAB FRAGMENT
632	1ae6	L	21	170	1e-79			164.95	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
632	1axz	L	21	170	1.7e-84			161.73	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY FAB', CATALYST, ALDOLASE REACTION
632	1b6d	A	21	170	1.5e-88	0.64	1.00		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
632	1bj1	L	21	170	1.2e-90	0.67	1.00		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
632	1bln	A	21	170	1.7e-85			165.55	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
632	1cly	L	23	170	2.7e-83			175.29	IGG FAB (HUMAN IGG1, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN CBR96 FAB (IMMUNOGLOBULIN); IMMUNOGLOBULIN, IMMUNOGLOBULIN C REGION, GLYCOPROTEIN, ANTIB
632	1clz	L	21	170	5.4e-84			165.08	IGG FAB (IGG3, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN MBR96 FAB (IMMUNOGLOBULIN); IMMUNOGLOBULIN C REGION, GLYCOPROTEIN, TRANSMEMBRANE
632	1dbb	L	21	170	1.1e-83			161.02	IMMUNOGLOBULIN FAB' FRAGMENT OF THE DB3 ANTI-STEROID MONOCLONAL	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
629	1ton		24	250	1.9e-91	0.74	1.00		HYDROLASE(SERINE PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) 1TON 4	
629	1ton		24	250	1.9e-91			201.47	HYDROLASE(SERINE PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) 1TON 4	
629	1trn	A	23	249	1.7e-92	0.92	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
629	1trn	A	24	250	1.7e-92			198.92	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
629	2tbs		23	250	8.5e-91	1.09	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ANTIBODY D2.3 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM
632	2fgw	L	21	170	6.8e-91	0.64	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY H52 (HUH52-OZ FAB) 2FGW 4	
633	1a2y	A	20	118	3.4e-33			51.12	MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
633	1a7q	L	20	118	1.7e-32			50.86	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, VARIANT
633	1ap2	A	20	118	1.7e-33			51.40	MONOCLONAL ANTIBODY C219; CHAIN: A, B, C, D;	IMMUNOGLOBULIN VARIABLE DOMAIN; SINGLE CHAIN FV, MONOCLONAL ANTIBODY, C219, P-GLYCOPROTEIN, 2 IMMUNOGLOBULIN
633	1bd2	E	22	117	5.1e-38	-0.18	0.99		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
633	1bec		23	117	3.4e-38	0.14	1.00		14.3.D T CELL ANTIGEN	RECEPTOR T CELL RECEPTOR 1BEC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ANTIBODY 1DBB 3 (IOG1, SUBGROUP 2A, KAPPA 1) COMPLEX WITH PROGESTERONE 1DBB 4	
632	1dee	A	21	170	1.7e-91	0.58	1.00		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
632	1fir	L	21	170	3.4e-86			169.43	4-4-20 (IG*G2A-KAPPA+) FAB FRAGMENT; 1FLR 5 CHAIN: L, H; 1FLR 6	IMMUNOGLOBULIN
632	1fvd	A	21	170	3.4e-89	0.57	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
632	1hil	A	21	169	3.4e-90	0.45	1.00		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	
632	1hil	A	21	170	3.4e-90			148.78	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	
632	1hyx	L	21	170	1.5e-84			165.42	IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
632	1ifh	L	21	169	3.4e-90	0.50	1.00		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF 1IFH 3 INFLUENZA HEMAGGLUTININ HA1	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	14
633	1bfv	L	20	118	8.5e-27			51.90	FV4155; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FV FRAGMENT, STEROID HORMONE, 2 FINE SPECIFICITY
633	1bj1	L	20	117	1.7e-38	-0.21	0.95		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
633	1bvk	A	20	118	6.8e-38			52.24	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
633	1dee	A	20	117	6.8e-40	-0.29	0.81		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
633	1dfb	L	20	118	3.4e-38	0.22	0.83		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
633	1dlf	L	20	117	1.7e-27			52.01	ANTI-DANSYL IMMUNOGLOBULIN IGG2A(S); CHAIN: L, H;	IMMUNOGLOBULIN ANTI-DANSYL FV FRAGMENT FV FRAGMENT, IMMUNOGLOBULIN
633	1dnf	L	20	118	3.4e-25			50.95	ANTICANCER ANTIBODY B1; CHAIN: L, H;	IMMUNOGLOBULIN B1DSFV; MONOCLONAL ANTIBODY, ANTITUMOR, IMMUNOGLOBULIN
633	1fgv	L	20	118	3.4e-40	-0.00	0.99		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(STRAIN X47) (RESIDUES 101-107) 1IFH 4	
632	1ifh	L	21	170	3.4e-90			148.62	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF 1IFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) 1IFH 4	
632	1igf	L	21	170	1.4e-83			163.94	IMMUNOGLOBULIN IGG1 FAB' FRAGMENT (B13I2) 1IGF 3	
632	1mcp	L	21	169	1e-93	0.69	1.00		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MC/PC603) 1MCP 4	
632	1mcp	L	21	170	1e-93			153.91	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MC/PC603) 1MCP 4	
632	1plg	L	21	170	3.4e-85			165.16	IGG2A-KAPPA+; 1PLG 4 CHAIN: L, H; 1PLG 5	IMMUNOGLOBULIN
632	1sbs	L	21	169	6.8e-95	0.64	1.00		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
632	1sbs	L	21	170	6.8e-95			151.88	MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
632	1yec	L	21	170	1.1e-82			153.63	IGG2A FAB FRAGMENT (D2.3); CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TRANSITION STATE ANALOGUE
632	1yej	L	21	170	1.1e-82			154.30	IG ANTIBODY D2.3 (LIGHT CHAIN); CHAIN: L; IG	IMMUNE SYSTEM ABZYME, TRANSITION STATE ANALOG,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HEMOGLOBIN THIONVILLE ALPHA CHAIN MUTANT WITH VAL 1 1BAB 3 REPLACED BY GLU AND AN ACETYLATED MET BOUND TO THE 1BAB 4 AMINO TERMINUS 1BAB 5	
635	1cb4	A	1	75	5.1e-35	-0.68	1.00		MODULE-SUBSTITUTED CHIMERA HEMOGLOBIN BETA-ALPHA; CHAIN: A, B, C, D;	OXYGEN TRANSPORT OXYGEN TRANSPORT, CHIMERA PROTEIN, RESPIRATORY PROTEIN, HEME
635	1fdh	G	1	77	1.7e-38	-0.70	1.00		OXYGEN TRANSPORT HEMOGLOBIN (DEOXY, HUMAN FETAL F=(11$=) 1FDHG 1 1FDHH 2	
635	1hbr	B	1	77	1e-35	-0.76	1.00		HEMOGLOBIN D; CHAIN: A, C; HEMOGLOBIN D; CHAIN: B, D;	OXYGEN STORAGE/TRANSPORT HB D; HB D HEMOGLOBIN D (R-STATE) 1, HEMOGLOBIN, AVIAN, HIGH 2 COOPERATITY, OXYGEN TRANSPORT
635	1hda	B	1	77	1.7e-33	-0.57	0.99		OXYGEN TRANSPORT HEMOGLOBIN (DEOXY) 1HDA 3	
635	1hds	B	1	77	6.8e-31	-0.73	0.93		OXYGEN TRANSPORT HEMOGLOBIN (SICKLE CELL) 1HDS 4	
635	1ibe	B	1	77	1.2e-36	-0.46	1.00		HEMOGLOBIN (DEOXY); CHAIN: A, B;	OXYGEN TRANSPORT HEME, OXYGEN TRANSPORT, RESPIRATORY PROTEIN, ERYTHROCYTE
635	1qpw	B	1	77	1.5e-34	-0.64	1.00		PORICINE HEMOGLOBIN (ALPHA SUBUNIT); CHAIN: A, C; PORICINE HEMOGLOBIN (BETA	OXYGEN TRANSPORT X-RAY STUDY, PORCINE HEMOGLOBIN, ARTIFICIAL HUMAN BLOOD, 2 OXYGEN TRANSPORT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									T1GI ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
633	1fgv	L	20	118	3.4e-40			54.70	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
633	1fvc	A	20	118	3.4e-40	-0.06	0.86		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
633	1fvc	A	20	118	3.4e-40			52.10	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
633	1fvd	A	20	118	6.8e-41	0.08	0.88		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
633	1ivl	A	20	117	3.4e-28			52.59	IMMUNOGLOBULIN IMMUNOGLOBULIN VL DOMAIN (VARIABLE DOMAIN OF KAPPA LIGHT 1IVL 3 CHAIN) OF DESIGNED ANTIBODY M39S 1IVL 4	
633	1maj		20	118	8.5e-27			54.30	IMMUNOGLOBULIN MURINE ANTIBODY 26-10 VL DOMAIN (NMR, 15 ENERGY MINIMIZED 1MAJ 3 STRUCTURES) 1MAJ 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SUBUNIT); CHAIN: B, D	
637	1a2y	A	19	131	1.7e-37			56.90	MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
637	1a7q	L	19	131	1e-35			57.44	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, VARIANT
637	1ad0	A	19	200	6.8e-56			51.63	FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
637	1adq	L	21	189	1.5e-76	0.19	0.81		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
637	1aqk	L	21	188	1.2e-68	0.05	0.74		FAB B7-13A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
637	1ar1	D	19	131	1.7e-33			52.73	CYTOCHROME C OXIDASE; CHAIN: A, B; ANTIBODY FV FRAGMENT; CHAIN: C, D;	COMPLEX (OXIDOREDUCTASE/ANTIBODY) CYTOCHROME AA3, COMPLEX IV, FERROCYTOCHROME C, COMPLEX (OXIDOREDUCTASE/ANTIBODY), ELECTRON TRANSPORT, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
633	1ctr	B	20	115	1.7e-38	0.00	1.00		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
633	2fgw	L	20	118	6.8e-40	-0.09	0.43		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-0Z FAB) 2FGW 4	
633	2imn		20	118	5.1e-34			50.13	IMUNOGLOBULIN IMMUNOGLOBULIN VL DOMAIN (VARIABLE DOMAIN OF KAPPA 2IMN 3 LIGHT CHAIN) OF MCPC603 MUTANT IN WHICH 2IMN 4 COMPLEMENTARITY-DETERMINING REGION 1 HAS BEEN REPLACED BY 2IMN 5 THAT FROM MOPC167 2IMN 6	
633	43c9	A	20	118	1.7e-33			52.37	IMMUNOGLOBULIN (LIGHT CHAIN); CHAIN: A, C, E, G; IMMUNOGLOBULIN (HEAVY CHAIN); CHAIN: B, D, F, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN
635	1a4f	B	1	77	1.7e-35	-0.66	1.00		HEMOGLOBIN; CHAIN: A, B	OXYGEN TRANSPORT OXYGEN TRANSPORT, HEME, RESPIRATORY PROTEIN, ERYTHROCYTE
635	1a9w	E	1	77	1.2e-36	-0.68	1.00		HEMOGLOBIN; CHAIN: A, B, C, F;	OXYGEN TRANSPORT OXYGEN TRANSPORT
635	1bab	B	1	77	1.7e-36	-0.71	1.00		OXYGEN TRANSPORT	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(/MCG5-/WEIRS HYBRID) 1MCW 4	
637	1ngp	H	19	200	1.5e-21			51.23	N109 (GG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
637	1qrn	D	20	200	1.4e-12			52.06	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
637	1tcr	A	20	200	6.8e-17			52.17	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
637	1wtd	A	19	131	8.5e-41			55.36	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
637	2fb4	L	20	188	1.2e-68	0.14	0.47		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB 2FB4 4	
637	2fgw	L	19	200	3.4e-57			52.58	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-0Z FAB) 2FGW 4	
637	2mcg	I	21	188	5.1e-68	0.12	0.31		IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (/MCG5) 2MCG 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										TRANSMEMBRANE, CYTOCHROME OXIDASE, ANTIBODY COMPLEX
637	1b0w	A	19	131	1.4e-39			53.76	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
637	1b6d	A	19	200	3.4e-55			50.36	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
637	1bd2	D	20	199	1.6e-09			51.40	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
637	1bj1	L	19	176	1.7e-57	0.21	0.64		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
637	1bj1	L	19	200	1.7e-57			52.82	FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
637	1bjm	A	21	188	8.5e-67	0.05	0.53		LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; 1BJM 8 BENCE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
637	1bvk	A	19	131	3.4e-41			54.69	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(TRIGONAL FORM) 2MCG 4	
637	2rhe		20	138	1e-47			55.78	IMMUNOGLOBULIN BENCE-*JONES PROTEIN (LAMBDA, VARIABLE DOMAIN) 2RHE 4	
637	8fab	A	23	189	1.7e-69	0.10	0.87		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN (GG1 (LAMBDA, HIL) 8FAB 3	
639	1a1b	A	1	84	1.2e-29			59.24	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
639	1a1b	A	28	110	1.2e-29	0.29	0.13		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
639	1a1b	A	2	82	1.2e-27	0.32	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
639	1a1b	A	2	84	5.4e-29	-0.17	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ANTIBODY/HYDROLASE)
637	1bww	A	17	132	1.7e-41			56.65	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
637	1ce1	L	19	200	1.2e-53			50.97	CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
637	1dfb	L	19	200	1.4e-54			54.95	IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
637	1fgv	L	19	131	3.4e-43			57.59	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
637	1igm	L	19	140	6.8e-42			55.75	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
637	1jrh	L	19	191	3.4e-43			56.16	ANTIBODY A6; CHAIN: L, H; INTERFERON-GAMMA RECEPTOR ALPHA CHAIN; CHAIN: I;	COMPLEX (ANTIBODY/ANTIGEN) CYTOKINE RECEPTOR, COMPLEX (ANTIBODY/ANTIGEN), 2 TRANSMEMBRANE, GLYCOPROTEIN
637	1lil	A	21	189	1.2e-70	0.12	0.43		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
637	1mcw	W	21	177	1.7e-59	0.00	-0.05		IMMUNOGLOBULIN IMMUNOGLOBULIN HETEROLOGOUS LIGHT CHAIN DIMER 1MCW 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, C; U2 B"; CHAIN: B, D;	RNA, SNRNP,RIBONUCLEOPROTEIN
640	1e9n	A	58	182	2.7e-22	0.50	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
640	1e9n	A	82	203	2.2e-17	0.00	-0.09		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
640	1e9n	C	40	159	1.4e-15	0.24	0.88		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
640	1e9n	C	58	182	1.4e-22	0.47	0.69		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
640	1e9n	C	82	203	1.4e-17	0.55	0.15		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
640	1ca6	A	248	374	5.4e-09	-0.18	0.06		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
640	1ca6	A	334	426	1.7e-08	0.10	-0.14		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
640	1d0b	A	26	204	1.7e-22	-0.20	0.01		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
640	1d0b	A	61	256	6.8e-22	0.18	0.09		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
640	1dce	A	24	111	8.5e-10	0.22	0.72		RAB GERANYLGERANYLTRAN	TRANSFERASE CRYSTAL STRUCTURE, RAB

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									BINDING SITE; CHAIN: D, C;	
639	1mey	C	1	83	3.4e-49			83.70	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
639	1mey	C	27	110	3.4e-49	0.14	0.71		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
639	1mey	C	2	82	6.8e-48	0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
639	1mey	G	55	82	3.4e-14	0.44	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
639	1tf6	A	2	112	5.1e-28	-0.56	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
639	1ubd	C	1	111	3.4e-32			58.78	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRAN SFERASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
640	1dce	A	52	183	1.7e-09	-0.04	0.84		RAB GERANYLGERANYLTRAN SFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRAN SFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
640	1dz9	A	20	135	3.4e-12	-0.33	0.17		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
640	1dz9	A	75	182	1.1e-13	-0.20	0.23		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
640	1ev2	E	340	372	1.7e-05	-0.76	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
640	1evt	C	340	372	1.7e-05	-0.73	0.05		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										(TRANSCRIPTION REGULATION/DNA)
639	1ubd	C	1	82	1.4e-28	0.09	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
639	1ubd	C	7	110	3.4e-32	-0.02	0.24		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
639	2adr		29	89	1e-15			51.76	ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
639	2gli	A	17	109	5.1e-29	0.13	-0.03		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
639	2gli	A	4	82	5.4e-24	0.02	0.18		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
640	1e4y	A	52	181	3.4e-13	-0.17	0.36		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
640	1e9n	A	40	152	1.6e-15	0.14	0.63		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A';	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA),

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
641	1mey	C	273	348	2.7e-23	-0.22	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
641	1mey	C	295	377	3.4e-51			78.38	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
641	1mey	C	296	376	3.4e-51	0.14	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
641	1mey	C	323	422	1.7e-47	-0.36	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
641	1tf3	A	295	380	5.1e-19			59.21	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
641	1tf6	A	271	424	3.4e-32	-0.14	0.12		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
641	1tf6	A	295	440	3.4e-32			69.98	TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
640	1fns		519	569	0.0027	0.08	0.35		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	
640	1fo1	A	45	111	1.7e-06	-0.15	0.11		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
640	1fo1	B	45	111	1.7e-06	-0.46	0.11		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
640	1fqv	A	52	192	1.4e-10	0.01	-0.03		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
640	1fs2	A	52	181	8.1e-16	0.02	0.23		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
640	2brn		52	183	1.6e-19	-0.09	0.29		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
641	1a1h	A	273	348	1.1e-21	-0.09	0.95		QQSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B,	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
641	1ubd	C	273	377	5.1e-35			87.61	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
641	1ubd	C	278	376	5.1e-35	-0.29	0.89		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
641	2gli	A	233	378	8.5e-31			77.15	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
641	2gli	A	246	378	8.5e-31	-0.27	0.40		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
646	1a14	L	20	126	3.4e-42			51.26	NEURAMINIDASE; CHAIN: N; SINGLE CHAIN ANTIBODY; CHAIN: H, L;	COMPLEX (ANTIBODY/ANTIGEN) COMPLEX (ANTIBODY/ANTIGEN), SINGLE-CHAIN ANTIBODY, 2 GLYCOSYLATED PROTEIN
646	1b0w	A	20	130	1.4e-49			51.14	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A,	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C;	
641	1a1h	A	296	376	3.4e-31	-0.27	0.99		QQSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
641	1a1h	A	296	379	3.4e-31			72.92	QQSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
641	1buo	A	5	127	1e-20			58.53	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
641	1buo	A	6	119	1e-20	-0.11	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
641	1mey	C	247	320	5.1e-37	0.03	0.21		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									MONOCLONAL ANTI-HEN EGG LYSOZYME ANTIBODY D11.15 COMPLEX WITH PHEASANT EGG LYSOZYME 1JHL 5 LYSOZYME 1JHL 6	
646	1nmb	L	20	130	5.1e-45			52.88	N9 NEURAMINIDASE; 1NMB 4 CHAIN: N; 1NMB 5 FAB NC10; 1NMB 9 CHAIN: L, H; 1NMB 10	COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
646	1tcr	A	21	130	5.1e-40			58.98	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
646	1wd	A	20	129	3.4e-49			50.85	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
646	2fgw	L	20	126	1e-53	0.28	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
648	1ao7	D	24	135	1.7e-40			119.10	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN:	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									B, C;	IMMUNE SYSTEM
646	1b6d	A	20	126	1.7e-51	0.21	1.00		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
646	1bj1	L	20	126	1.7e-53	0.35	1.00		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
646	1bvk	A	20	130	1.7e-49			54.02	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
646	1bww	A	18	129	1e-51			51.17	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
646	1bww	A	20	127	1e-51	0.23	1.00		IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
646	1ca1	L	20	126	5.1e-50	0.37	0.96		CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
646	1dee	A	20	126	1.2e-54	0.18	1.00		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IIIF COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									E;	
648	1ao7	D	25	137	1.7e-40	0.45	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
648	1b88	A	23	131	1.7e-42			77.78	T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	T CELL RECEPTOR TCR; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
648	1b88	A	24	133	1.7e-42	0.48	1.00		T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	T CELL RECEPTOR TCR; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
648	1bd2	D	24	137	1e-42	0.53	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
648	1bwm	A	24	134	3.4e-44	0.22	1.00		ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
648	1d9k	A	23	134	3.4e-43	0.34	1.00		T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A, E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B, F; MHC I-AK A	IMMUNE SYSTEM MHC I-AK; MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										SPECIFICITY
646	1dfb	L	20	126	6.8e-50	0.22	1.00		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
646	1fgv	L	20	126	3.4e-53	0.43	0.94		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
646	1fgv	L	20	129	3.4e-53			57.39	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
646	1fvc	A	20	126	3.4e-50	0.33	0.98		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
646	1fvc	A	20	130	3.4e-50			53.42	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
646	1fvd	A	20	126	1.2e-50	0.32	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
646	1jhl	L	20	130	1.5e-44			52.05	COMPLEX(ANTIBODY-ANTIGEN) FV FRAGMENT (IGG1, KAPPA) (LIGHT AND HEAVY VARIABLE DOMAINS 1JHL 3 NON-COVALENTLY ASSOCIATED) OF	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
649	1cc1	L	21	237	3.4e-82			81.96	CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
649	1cly	L	22	240	5.1e-73			84.78	IGG FAB (HUMAN IGG1, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN CBR96 FAB (IMMUNOGLOBULIN); IMMUNOGLOBULIN, IMMUNOGLOBULIN C REGION, GLYCOPROTEIN, ANTIB
649	1clz	L	20	229	3.4e-75			82.55	IGG FAB (IGG3, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN MBR96 FAB (IMMUNOGLOBULIN); IMMUNOGLOBULIN C REGION, GLYCOPROTEIN, TRANSMEMBRANE
649	1cl8	A	21	229	1.7e-74			81.49	7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
649	1dee	A	20	229	3.4e-88	-0.04	0.84		IGM RF 2A2; CHAIN: A, C, E; IGM RF 3A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
649	1fgn	L	21	229	1.2e-80			81.24	IMMUNOGLOBULIN FAB 5G9; CHAIN: L, H;	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE, IMMUNOGLOBULIN
649	1fns	L	20	229	3.4e-84	-0.27	0.75		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN),

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WILLEBRAND FACTOR; CHAIN: A;	BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
649	1fvd	A	20	229	5.1e-85	0.27	0.75		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
649	1gc1	L	21	237	6.8e-80			82.59	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
649	1igt	A	20	229	1e-84	-0.01	0.53		1003A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
649	1lil	A	21	229	1.5e-66			81.70	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
649	1qrn	D	21	226	1.7e-55			224.26	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
649	1stn	L	20	229	8.5e-84	-0.03	0.65		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
649	1tcr	A	21	231	2.7e-74			237.84	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
649	1vge	L	22	229	8.5e-84	0.14	0.62		TRI.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TRI.9, ANTI-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN (ALPHA CHAIN); CHAIN: C, G; MHC I-AK B CHAIN (BETA CHAIN); CHAIN: D, H; CONALBUMIN PEPTIDE; CHAIN: P, Q;	
648	1kb5	A	24	133	1e-44	0.68	1.00		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
648	1kb5	A	24	133	1e-44			74.20	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
648	1qrn	D	24	142	1.7e-40			74.24	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
648	1qrn	D	25	137	1.7e-40	0.49	1.00		MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
649	1a6j	L	21	238	1e-73			82.63	IMMUNOGLOBULIN,	IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
649	1ac6	L	21	229	8.5e-73			83.03	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
649	1b2w	L	20	229	5.1e-85	0.01	0.58		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
649	1b2w	L	21	240	5.1e-85			85.20	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
649	1b4j	L	21	240	5.1e-79			81.22	ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
649	1b6d	A	20	227	5.1e-84	0.15	0.70		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
649	1bj1	L	20	228	3.4e-86	-0.04	0.54		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FRAGMENT; CHAIN: B;	
650	1fbi	H	21	247	5.1e-91	0.48	0.99		COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (IGG1) 1FBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FBI 4	
650	1fvd	B	21	250	5.1e-92	0.38	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
650	1igc	H	21	250	1e-92	0.42	1.00		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) 1IGC 5 PROTEIN G, STREPTOCOCCUS 1IGC 15	
650	1ig2	B	21	258	5.1e-95	0.28	1.00		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
650	1lmk	A	8	134	6.8e-32	0.16	0.53		IMMUNOGLOBULIN ANTI-PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE-CHAIN FV DIMER 1LMK 4	
650	1ngp	H	21	247	1.4e-94	0.66	1.00		N1G9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
649	2fgw	L	20	229	3.4e-87	-0.04	0.52		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
649	2fgw	L	21	229	3.4e-87			83.47	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
649	6fab	L	21	229	3.4e-80			81.24	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT OF THE MURINE ANTI-PHENYLARSONATE 6FAB 3 ANTIBODY 36-71, FAB 36-71 6FAB 4	
650	1ac6	H	21	245	1.4e-91	0.55	1.00		ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
650	1afv	H	21	247	5.1e-93	0.57	1.00		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
650	1ao7	E	23	264	8.5e-62			303.44	HLA-A 0201; CHAIN: A;	COMPLEX (MHC/VIRAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
650	1aqb	A	11	135	6.8e-33	0.07	0.92		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
650	1qok	A	11	134	8.5e-37	0.39	0.98		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
650	1wej	H	21	250	5.1e-91	0.35	1.00		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
652	1ccd		1	58	0.0019	-0.41	0.43		PHOSPHOLIPASE A2 INHIBITOR CLARA CELL 17.KDA PROTEIN 1CCD 3	
652	1utg		3	58	0.0016	0.07	0.09		STEROID BINDING UTEROGLOBIN (OXIDIZED) 1UTG 4	
656	1bu7	A	1	373	2.7e-60	0.40	1.00		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
656	1bu7	A	1	385	1.7e-45	0.40	1.00		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
656	1bu7	A	1	408	2.7e-60			114.08	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	PEPTIDE/RECEPTOR) HLA-A3 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
650	1bd2	E	23	264	1.7e-84			397.14	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
650	1bcc		23	264	5.4e-95			324.99	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
650	1bec		24	263	5.4e-95	0.73	1.00		14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
650	1dzb	A	9	134	8.5e-35	0.34	0.82		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
650	1e6o	H	21	247	5.1e-92	0.49	1.00		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
650	1f3r	B	17	134	1.5e-33	0.11	0.89		ACETYLCHOLINE RECEPTOR ALPHA; CHAIN: A; FV ANTIBODY	IMMUNE SYSTEM IG-FOLD, IMMUNO COMPLEX, ANTIBODY-ANTIGEN, BETA-TURN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
659	1tf6	A	97	273	1e-32			57.65	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
659	1ubd	C	105	211	8.5e-30	-0.67	0.04		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
659	1ubd	C	135	244	6.8e-31	-0.65	0.01		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
659	1ubd	C	165	269	2.7e-10	-0.44	0.16		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
659	2gli	A	138	273	6.8e-32	-0.41	0.01		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
659	2gli	A	94	246	6.8e-32			59.77	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
656	1cpt		149	390	1e-16	0.03	0.42		OXIDOREDUCTASE(OXYGENASE) CYTOCHROME P450-TERP 1CPT 3	
656	1dt6	A	2	388	0	0.49	1.00		CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYP2C5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
656	1f26	A	6	373	1.3e-50	0.14	0.47		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
656	1f26	A	91	384	1.7e-07	-0.28	0.00		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
656	1f4t	A	22	373	8.1e-31	-0.16	0.25		CYTOCHROME P450 119; CHAIN: A, B;	OXIDOREDUCTASE CYP119; P450 FOLD
656	1oxa		1	373	5.4e-61	-0.05	0.99		CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
656	1oxa		1	399	3.4e-61			79.88	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
656	1oxa		9	384	1.7e-19	0.26	0.95		CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
656	1qmq	A	146	388	1.4e-06	0.03	0.27		CYTOCHROME P450; CHAIN: A;	OXIDOREDUCTASE CAMPHOR 5-MONOOXYGENASE OXIDOREDUCTASE(OXYGENASE), RU-SUBSTRATE,
658	1b34	A	1	52	1.1e-11	-0.33	0.00		SMALL NUCLEAR RIBONUCLEOPROTEIN SM	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
664	1ads		11	129	6.8e-42	0.56	1.00		OXIDOREDUCTASE ALDOSE REDUCTASE (E.C.1.1.1.21) COMPLEX WITH NADPH 1ADS 3	
664	1afs	A	8	129	1.7e-38	0.54	1.00		3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA-HSD; OXIDOREDUCTASE, NAD
664	1ab4		8	128	3.4e-39	0.51	1.00		ALDOSE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
664	1c9w	A	9	128	3.4e-39	0.55	1.00		CHO REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALPHA/BETA TIM BARREL, PROTEIN-NADP+ COMPLEX
664	1cil	A	11	129	6.8e-42	0.50	1.00		ALDOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALDOSE REDUCTASE, INHIBITION, DIABETES
664	1frb		9	128	6.8e-39	0.57	1.00		FR-1 PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE (NADP) ALDO-KETO OXIDOREDUCTASE (NADP), TIM BARREL
666	1c3t	A	1	55	8.5e-26	-0.62	0.42		1D8 UBIQUITIN; CHAIN: A;	DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITIN, DE NOVO PROTEIN, UBIQUITIN
666	1tbe	B	1	55	1e-27	-0.48	0.59		UBIQUITIN TETRAUBIQUITIN 1TBE 3	
666	1ubi		1	55	1e-27	-0.52	0.60		CHROMOSOMAL PROTEIN UBIQUITIN 1UBI 3	
666	1ud7	A	1	55	5.1e-26	-0.71	0.34		UBIQUITIN CORE MUTANT 1D7; CHAIN: A;	UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT
671	1zls	L	18	227	1.7e-68			73.68	2E8 (IGG1-KAPPA) ANTIBODY; CHAIN: L, H,	IMMUNOGLOBULIN IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE
658	1d3b	B	3	51	5.1e-12	0.14	-0.12		SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN
659	1a1h	A	160	244	1.7e-26	-0.26	0.13		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
659	1a1h	A	98	185	1.7e-26	-0.52	0.09		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
659	1mey	C	159	244	5.1e-46	-0.57	0.46		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
659	1mey	G	217	244	1.7e-13	-0.52	0.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									IMMUNOGLOBULIN	
671	2sc8	L	18	225	1.5e-73			74.57	1OG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
671	2mcg	I	17	226	6.8e-63			75.07	IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (/MCG5) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
671	7fab	L	18	222	1e-59			76.52	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
671	1adq	L	19	242	8.5e-57			67.94	IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
671	1aif	L	18	240	5.1e-63	0.26	0.25		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
671	1ao7	E	18	250	3.4e-27			69.03	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
671	1bd2	E	18	250	1.7e-38			77.88	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									M, P;	
671	1aif	L	17	227	5.1e-72			73.37	ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
671	1bbj	L	17	222	5.1e-69			72.88	IMMUNOGLOBULIN FAB' FRAGMENT OF MONOCLONAL ANTIBODY B72.3 1BBJ 3 (MURINE/HUMAN CHIMERA) 1BBJ 4	
671	1bd2	E	18	234	1.2e-22			72.64	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
671	1bec		18	234	1.7e-21			75.74	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
671	1bih	A	17	403	8.5e-16			102.10	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
671	1ce1	L	17	222	5.1e-72			72.55	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
671	1fig	L	18	227	3.4e-72			73.31	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT 1FIG 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	PEPTIDE/RECEPTOR)
671	1bec		18	250	1.7e-32			76.74	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
671	1bih	A	17	419	2.7e-36			90.93	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
671	1bj1	L	18	240	6.8e-63	0.26	0.13		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
671	1bjm	A	17	242	1.5e-34			67.92	LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; 1BJM 8 BENCE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
671	1bvk	A	18	119	3.4e-33	0.24	0.00		HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
671	1bww	A	18	118	1.7e-32	0.81	-0.05		IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
671	1cdy		254	331	5.4e-14	0.20	0.35		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
671	1fvd	A	17	225	8.5e-72			76.29	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
671	1kb5	L	17	227	6.8e-72			73.99	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
671	1nca	L	18	227	8.5e-72			73.83	HYDROLASE(O-GLYCOSYL) N9 NEURAMINIDASE-NC41 (E.C.3.2.1.18) COMPLEX WITH FAB 1NCA 3	
671	1nfd	B	18	235	6.8e-25			77.54	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
671	1osp	L	17	227	5.1e-67			73.22	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSPA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB 184.1, BORRELIA BURGDORFERI 3 STRAIN B31
671	1tcr	B	18	235	5.1e-22			73.74	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
671	1vge	L	17	225	8.5e-72			75.01	TRI.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TRI.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									AA FV) 1FGV 4	
671	1ffg	L	20	240	5.1e-63	0.17	0.27		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB FRAGMENT 1FIG 3	
671	1ffm	L	18	240	3.4e-63	0.36	0.12		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 2B VON WILLEBRAND DISEASE
671	1fvc	A	18	120	1.2e-32	0.65	-0.14		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
671	1fvd	A	17	241	6.8e-61			66.39	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
671	1hng	A	159	338	1.9e-18	0.08	-0.14		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	
671	1igm	L	18	126	8.5e-34	0.46	-0.01		IMMUNOGLOBULIN IMMUNOGLOBULIN M (10-M) FV FRAGMENT 1IGM 3	
671	1ilb	B	139	420	1.9e-14			69.14	INTERLEUKIN-1 BETA; CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
671	1ilb	B	154	362	1.9e-14	0.34	0.09		INTERLEUKIN-1 BETA;	COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CELL SURFACE GLYCOPROTEIN
671	1cfb	L	20	240	3.4e-63	0.31	-0.03		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
671	1cvs	C	135	334	6.8e-47	0.37	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
671	1cvs	D	135	334	1e-48	0.33	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
671	1dzb	A	139	288	1.4e-12	0.19	-0.19		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
671	1epf	A	159	334	5.4e-17	0.41	0.92		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
671	1ev2	E	132	334	1.7e-45	0.36	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
671	1ev2	E	265	344	5.1e-14	0.30	0.28		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
671	1mcp	L	19	240	8.3e-63	0.44	0.06		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MCPC603) 1MCP 4	
671	1nct		255	331	8.1e-15	0.44	0.07		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
671	1nfd	B	18	251	5.1e-35			76.63	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
671	1qac	A	19	119	1.7e-32	0.55	-0.05		IMMUNOGLOBULIN LIGHT CHAIN VARIABLE DOMAIN; CHAIN: A, B;	IMMUNE SYSTEM BETA BARREL IMMUNOGLOBULIN VL DOMAIN DIMER, FLIPPED DOMAIN 2 DIMER
671	1qnz	L	20	119	1.7e-31	0.37	0.06		0.5B ANTIBODY (LIGHT CHAIN); CHAIN: L; 0.5B ANTIBODY (HEAVY CHAIN); CHAIN: H; GP120; CHAIN: P;	ANTIBODY ANTIBODY, V3 PEPTIDE, BINDING SITE
671	1sbn	L	19	240	3.4e-63	0.42	0.03		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
671	1tcr	B	18	251	1.7e-33			70.09	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
671	1ev2	G	134	338	1.4e-48	0.40	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
671	1evt	C	135	334	5.1e-49	0.40	-0.08		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
671	1evt	C	247	339	5.4e-14	0.62	0.16		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
671	1f6a	A	159	339	2.4e-14	0.35	-0.01		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-PC
671	1fgv	L	18	118	1.4e-34	0.29	-0.05		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 31/52' (11/H52-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
671	7fab	L	18	238	1.7e-53			68.11	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
672	12e8	L	18	227	1.7e-68			73.68	2E8 (IGG1-KAPPA-) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
672	1aif	L	17	227	5.1e-72			73.37	ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
672	1bbj	L	17	222	5.1e-69			72.88	IMMUNOGLOBULIN FAB' FRAGMENT OF MONOCLONAL ANTIBODY B72.3 1BBJ 3 (MURINE/HUMAN CHIMERA) 1BBJ 4	
672	1bd2	E	18	234	1.2e-22			72.64	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
672	1bec		18	234	1.7e-21			75.74	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
672	1blh	A	17	403	8.5e-16			102.10	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										SIGNAL
671	1tnm		255	331	2.7e-15	0.55	0.06		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) I TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) I TNM 4 I TNM 5B	
671	1wcj	L	18	240	8.5e-63	0.34	0.05		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: P;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
671	1wio	A	23	365	1.4e-25			78.38	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
671	1wit		257	331	1.1e-14	0.51	-0.15		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
671	1wti	A	18	119	6.8e-32	0.51	-0.11		IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN I WTL 3 (BENCE-JONES PROTEIN) I WTL 4	
671	25c8	L	20	240	1.7e-63	0.39	0.04		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
671	2dil	A	159	333	1.1e-14	0.05	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										HOMOPHILIC ADHESION
672	1cn1	L	17	222	5.1e-72			72.55	CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
672	1fig	L	18	227	3.4e-72			73.31	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT 1FIG 3	
672	1fvd	A	17	225	8.5e-72			76.29	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
672	1hh5	L	17	227	6.8e-72			73.99	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
672	1nca	L	18	227	8.5e-72			73.83	HYDROLASE(O-GLYCOSYL) N9 NEURAMINIDASE-NC41 (E.C.3.2.1.18) COMPLEX WITH FAB 1NCA 3	
672	1nfd	B	18	235	6.8e-25			77.34	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
672	1osp	L	17	227	5.1e-67			73.32	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSPA; COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
671	2fgw	L	18	240	3.4e-63	0.42	0.42		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 1H52' (1H52-OZ FAB) 2FGW 4	
671	2imm		19	119	1e-31	0.69	0.28		IMUNOGLOBULIN IMMUNOGLOBULIN VL DOMAIN (VARIABLE DOMAIN OF KAPPA 2IMN 3 LIGHT CHAIN) OF MCPC603 MUTANT IN WHICH 2IMN 4 COMPLEMENTARITY-DETERMINING REGION 1 HAS BEEN REPLACED BY 2IMN 5 THAT FROM MOPC167 2IMN 6	
671	2mcg	I	17	242	5.1e-56			68.68	IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG5) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
671	2ncm		255	338	5.4e-15	1.06	0.18		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
671	3ncm	A	255	331	5.4e-15	0.51	0.34		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
672	1bww	A	18	118	1.7e-32	0.81	-0.05		IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
672	1cdy		254	331	5.4e-14	0.20	0.35		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
672	1cf8	L	20	240	3.4e-63	0.31	-0.03		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
672	1cvs	C	135	334	6.8e-47	0.37	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
672	1cvs	D	135	334	1e-48	0.33	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
672	1dzb	A	139	288	1.4e-12	0.19	-0.19		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										(IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELIA BURGDORFERI 3 STRAIN B31
672	1cr	B	18	235	5.1e-22			73.74	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
672	1vgs	L	17	225	8.5e-72			75.01	TRI.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TRI.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
672	25c8	L	18	225	1.5e-73			74.57	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
672	2mcg	I	17	226	6.8e-63			75.07	IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG5) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
672	7fab	L	18	222	1e-59			76.52	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
672	1adq	L	19	242	8.5e-57			67.94	IGG4 RIA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
672	1alf	L	18	240	5.1e-63	0.26	0.25		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										SINGLE-CHAIN FV FRAGMENT
672	1cpf	A	159	334	3.4e-17	0.41	0.92		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
672	1ev2	E	132	334	1.7e-45	0.36	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
672	1ev2	E	265	344	5.1e-14	0.30	0.28		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
672	1ev2	G	134	338	1.4e-48	0.40	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
672	1evt	C	135	334	5.1e-49	0.40	-0.08		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
672	1evt	C	247	339	3.4e-14	0.62	0.16		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
672	1eo7	E	18	250	3.4e-27			69.03	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
672	1bd2	E	18	250	1.7e-38			77.88	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
672	1bec		18	250	1.7e-32			76.74	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
672	1bih	A	17	419	2.7e-36			90.93	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
672	1bj1	L	18	240	6.8e-63	0.26	0.13		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
672	1bjm	A	17	242	1.3e-54			67.92	LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; 1BJM 8 BENCE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
672	1bvk	A	18	119	3.4e-33	0.24	0.00		HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
672	1fbn	A	139	339	2.4e-14	0.35	-0.01		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR, CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCGEPSILON) IGE-FC, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
672	1fgv	L	18	118	1.4e-34	0.29	-0.05		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 7157 (HUH52-AA FV) IFGV 4	
672	1fig	L	20	240	5.1e-63	0.17	0.27		IMMUNOGLOBULIN (IMMUNOGLOBULIN G1 KAPPA LIGHT CHAIN) (IGG1 KAPPA) FAB FRAGMENT (1FIG)	
672	1fnn	A	18	240	3.4e-63	0.36	0.12		IMMUNOGLOBULIN (IMMUNOGLOBULIN G1 (KAPPA (KAPPA) LIGHT CHAIN)) 4 (GO1); CHAIN: L; IMMUNOGLOBULIN (IMMUNOGLOBULIN G1 (KAPPA (KAPPA) LIGHT CHAIN)) 4 (GO1); CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A-ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
672	1fvc	A	18	120	1.2e-32	0.65	-0.14		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 1 IFVC 3	
672	1fvd	A	17	241	6.8e-61			66.39	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
672	1hag	A	139	338	1.9e-18	0.08	-0.14		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
672	1fgn	L	18	126	8.5e-34	0.46	-0.01		IMMUNOGLOBULIN IMMUNOGLOBULIN M (GO-M) FV FRAGMENT 1IGM 3	
672	1ifb	B	139	420	1.9e-14			69.14	INTERLEUKIN-1 BETA; CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
672	1ifb	B	154	362	1.9e-14	0.34	0.09		INTERLEUKIN-1 BETA; CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
672	1mcp	L	19	240	8.5e-63	0.44	0.06		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MOPC860) 1MCP 4	
672	1nsf	B	18	251	5.1e-35	0.44	0.07		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN45, CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BACTERIAL IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
672	1nfd	B	18	251	5.1e-35			76.63	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
672	1qac	A	19	119	1.7e-32	0.55	-0.05		IMMUNOGLOBULIN LIGHT CHAIN VARIABLE	IMMUNE SYSTEM BETA BARREL IMMUNOGLOBULIN VL DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
672	1qas	L	20	119	1.7e-31	0.37	0.06		DOMAIN; CHAIN: A, B; 0.3B ANTIBODY (LIGHT CHAIN); CHAIN: L; 0.3B ANTIBODY (HEAVY CHAIN); CHAIN: H; GP120; CHAIN: P;	DIMER, FLIPPED DOMAIN 3 DIMER, ANTIBODY ANTIBODY, V3 PEPTIDE, BINDING SITE
672	1tbn	L	19	240	3.4e-63	0.42	0.03		MONOCLONAL ANTIBODY 3A6; CHAIN: H, L;	MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
672	1tcr	B	18	251	1.7e-33			70.09	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR, T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
672	1tnn		235	331	2.7e-15	0.55	0.06		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) (TNM 3) (NMR, MINIMIZED AVERAGE STRUCTURE) (TNM 4 (TNM 5)	
672	1wej	L	18	240	8.5e-63	0.34	0.05		E5 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: P;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E5, CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
672	1wio	A	23	365	1.4e-25			78.38	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
672	1wk		237	331	1.1e-14	0.51	-0.15		TWITCHIN 18TH 105P MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, 1 SET, MUSCLE PROTEIN
672	1wtf	A	18	119	6.8e-32	0.51	-0.11		IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FROM IMMUNOGLOBULIN LIGHT-CHAIN (WTL 3 (BENCE-JONES PROTEIN) WTL 4	
672	2hc4	L	20	240	1.7e-63	0.39	0.04		10G 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
672	2nll	A	139	333	1.1e-14	0.05	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
672	2qfw	L	18	240	3.4e-63	0.42	0.42		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 7157 (HUH52-OZ FAB) 2FGW 4	
672	2imm		19	119	1e-31	0.69	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN VL DOMAIN (VARIABLE DOMAIN OF KAPPA 2D4N 3 LIGHT CHAIN OF IMMUNOGLOBULIN M WHICH 2D4N 4 COMPLEMENTARITY-DETERMINING REGION 1 HAS BEEN REPLACED BY 2D4N 3 THAT FROM MOPC167 2D4N 6	
672	2mcg	1	17	242	5.1e-56			68.68	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN	IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DIMER (MCG5) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
672	2ncm		255	338	5.4e-15	1.06	0.18		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
672	3ncm	A	255	331	5.4e-15	0.51	0.34		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
672	7fab	L	18	238	1.7e-53			68.11	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
678	1got	A	6	264	6.8e-100			262.16	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
678	1tad	A	27	264	8.5e-95			271.77	GTP-BINDING PROTEIN TRANSDUCIN-ALPHA (GT-ALPHA-GDP-ALF, T-ALPHA-GDP-ALF) 1TAD 3 COMPLEXED WITH GDP AND ALUMINUM	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
679	1bwm	A	16	136	3.4e-36	0.18	0.90		ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
679	1d9k	A	22	136	8.5e-35	0.30	0.66		T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A, E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B, F; MHC I-AK A CHAIN (ALPHA CHAIN); CHAIN: C, G; MHC I-AK B CHAIN (BETA CHAIN); CHAIN: D, H; CONALBUMIN PEPTIDE; CHAIN: P, Q;	IMMUNE SYSTEM MHC I-AK; MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK
679	1fyt	D	21	136	8.5e-33	0.37	1.00		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DR1, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
679	1kb5	A	21	139	8.5e-37	0.24	0.13		KB5-C20 T-CELL ANTIGEN	COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FLUORIDE ITAD 4	
679	1ac6	A	21	123	8.5e-33			67.32	T-CELL RECEPTOR ALPHA; CHAIN: A, B;	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED MUTAGENESIS, 2 THREE-DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
679	1ac6	A	21	136	8.5e-33	0.45	1.00		T-CELL RECEPTOR ALPHA; CHAIN: A, B;	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED MUTAGENESIS, 2 THREE-DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
679	1ao7	D	21	132	3.4e-31			51.63	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
679	1ao7	D	23	136	3.4e-31	-0.07	0.89		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
679	1b88	A	21	136	1.5e-34	0.17	0.53		T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	T CELL RECEPTOR TCR; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
679	1bd2	D	21	136	1.7e-34	0.40	0.89		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI BLAST Score	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	(IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
679	1qrn	D	23	136	3.4e-31	0.34	0.72		MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE PSA; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T2 CELL RECEPTOR, IMMUNE SYSTEM
679	1tcr	A	21	127	1.2e-32	0.37	0.98		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
679	1tcr	A	21	146	1.2e-32			51.61	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
680	1scs	A	70	138	0.0027	0.01	0.06		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	
680	4hb1		164	207	5.1e-05	0.56	0.01		DHP1; CHAIN: NULL;	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE

TRA 1595601v1

TABLE 6

SEQ ID NO:	Position of The Last Amino Acid of The Signal	Maximum Score	Mean Score
342	1-13	0.981	0.764
343	1-46	0.978	0.754
344	1-34	0.954	0.756
345	1-45	0.981	0.651
346	1-22	0.982	0.882
347	1-13	0.981	0.764
348	1-27	0.992	0.969
349	1-15	0.909	0.589
350	1-33	0.961	0.864
351	1-17	0.974	0.943
353	1-20	0.957	0.874
354	1-20	0.972	0.771
355	1-28	0.941	0.755
356	1-22	0.932	0.802
357	1-20	0.895	0.595
358	1-17	0.884	0.588
359	1-16	0.988	0.881
360	1-26	0.937	0.784
361	1-29	0.981	0.864
362	1-26	0.968	0.806
363	1-22	0.968	0.806
364	1-29	0.956	0.765
365	1-21	0.992	0.929
370	1-46	0.978	0.754
380	1-34	0.954	0.756
391	1-31	0.960	0.773
399	1-45	0.981	0.652
408	1-22	0.982	0.882
409	1-42	0.993	0.715
411	1-30	0.966	0.767
423	1-18	0.997	0.971
430	1-13	0.981	0.764
435	1-45	0.890	0.631
438	1-27	0.992	0.969
466	1-33	0.961	0.864
472	1-45	0.987	0.658
473	1-20	0.992	0.967
502	1-20	0.957	0.874
503	1-21	0.989	0.945
506	1-42	0.980	0.577
511	1-20	0.972	0.771
516	1-28	0.941	0.755
517	1-28	0.941	0.755
518	1-12	0.907	0.779
522	1-21	0.958	0.779
527	1-15	0.970	0.875
538	1-20	0.895	0.595
542	1-31	0.987	0.895
545	1-30	0.971	0.889
552	1-17	0.884	0.588
562	1-23	0.965	0.817
564	1-29	0.933	0.725
575	1-28	0.972	0.870

SEQ ID NO:	Position of The Last Amino Acid of The Signal	Maximum Score	Mean Score
577	1-17	0.966	0.905
586	1-26	0.921	0.587
595	1-20	0.938	0.631
606	1-18	0.901	0.763
611	1-20	0.940	0.693
613	1-26	0.937	0.784
617	1-22	0.972	0.745
618	1-15	0.930	0.748
619	1-35	0.906	0.600
622	1-29	0.981	0.864
629	1-19	0.976	0.916
630	1-27	0.973	0.951
631	1-29	0.950	0.629
632	1-19	0.969	0.913
633	1-21	0.956	0.823
637	1-17	0.976	0.938
640	1-18	0.991	0.978
645	1-26	0.968	0.806
646	1-20	0.972	0.828
647	1-27	0.893	0.567
648	1-21	0.994	0.959
649	1-20	0.945	0.891
650	1-21	0.984	0.858
651	1-27	0.891	0.593
654	1-40	0.955	0.703
668	1-22	0.968	0.806
671	1-23	0.982	0.945
672	1-23	0.982	0.945
675	1-32	0.955	0.617
676	1-23	0.936	0.677
679	1-20	0.937	0.859
680	1-29	0.956	0.765
681	1-23	0.968	0.819

TABLE 7

SEQ ID NO:	Chromosomal Location
1	17
2	10
3	11
4	4
5	15q25
6	3
7	3
9	12
11	12
12	17ptcr-p13.1
13	11
14	16p13.3
15	1
16	12p13
17	21q22.3
20	14
21	7q22
22	9
23	5q31
24	8p23-p22
25	11
26	X
27	X
28	15q14
29	10q24
30	17q21
31	11
32	8
33	5q34
34	6
35	10
37	8q24
40	4q13.3
41	10
44	20q11.22-q12
46	12
47	4
48	19
49	19
50	4
51	17
52	14
55	1
56	11
57	17p13.3
58	5p14.2-q31.3
59	7q11.2
60	15
61	19q13.3
62	6
63	5
64	7
65	22
66	12q24.3

SEQ ID NO:	Chromosomal Location
69	15
70	22q13.2
71	16
72	7q31.1
75	10
76	18
77	15
78	18q
79	6q14
80	11p15
81	5p13.3-q21.3
83	7q33
84	1q32
85	14
87	11q12-q13.1
89	22
90	1
91	1p36.13
92	7p14
93	10cen-q26.11
94	19
95	17
96	22q11.2
97	6q22.3
98	3
99	8
100	11
101	2
102	7p13-p11.2
103	15q21-q22
104	15
105	9q22.1-q22.3
106	Xq13.1
107	20
108	5
109	5
110	16q23
111	1p32-p35
112	9
113	Xq22
114	15
115	8q22-q23
117	6p21.3
118	16p13.3
119	15
120	16
121	2q37
123	8q22-q23
124	19q13.1
126	20p12.2-p11.22
127	8
128	12ptcr-p13.31
129	12ptcr-p13.31
131	18p11.22-p11.21
133	1q32.3-q41
134	19q13.4

SEQ ID NO:	Chromosomal Location
135	16
136	17
137	17pter-p13.1
139	7
140	8
141	Xp11.4-p11.21
142	1
143	6
144	5p14-15
145	14
146	14
147	20
148	22
149	19
150	17
151	15
152	15
154	6
155	10
156	12pter-p13.31
160	5p15.2
161	14q11.2
162	7q35
163	13
164	12
166	6q
168	18
169	7
170	7
171	6p12.1-21.1
172	6p12.1-21.1
173	15q22.1-q22.31
175	22q13.1
176	22q13.1
177	22q13.2-q13.31
178	11cen-q12.1
179	5
180	11
184	17q21.3
185	11
188	20
189	10
190	4p16
191	4
192	4
193	12
194	9
196	17p11.2
197	6
198	5
199	17
200	6q16.1-q16.3
202	1
203	2q13
205	19
209	19

SEQ ID NO:	Chromosomal Location
211	19
212	q25-26
216	19q13.3
217	21q11.2
218	Xq21.3-q22
219	6
221	14q11.2
222	5q32
224	13
225	3q13.3-q21
226	6q23-q24
227	17
228	17
231	14
232	22
233	19
234	5q11.2
237	7q22
241	19
242	15
244	1p22
246	3p21.1-9
248	p12.2-13
249	10
250	19p13.3
251	19p13.3
253	4
255	10
259	9
260	5q31
262	8
264	1q32.1-q41
267	10
269	11
272	5q34
274	19
275	3
279	17
280	2
286	22q13.1
287	7
288	19q13.3-q13.4
291	2p12
292	14
293	14q31
294	11p15.5
296	7p14-p13
298	7q35-q36
299	20
300	9
302	7q22
305	14q11.2
306	11
307	14q11.2
308	14q11.2
309	7q35

SEQ ID NO:	Chromosomal Location
313	p34.3-36.11
315	17
316	15
317	12
318	22q11.2
319	6pter-p22.1
322	22q
323	10
326	X
328	1
329	14q11.2
330	6p21.3
331	6p21.3
332	19q13.3
333	X
334	7q31.3-q32
337	3p21.3
338	14q11.2
339	9
341	2

TABLE 8

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
1	342	1
2	343	4
3	344	5
4	345	7
5	346	8
6	347	10
7	348	11
8	349	12
9	350	13
10	351	14
11	352	15
12	353	17
13	354	18
14	355	19
15	356	20
16	357	21
17	358	22
18	359	25
19	360	29
20	361	30
21	362	32
22	363	34
23	364	36
24	365	37
25	366	38
26	367	39
27	368	40
28	369	41
29	370	42
30	371	43
31	372	44
32	373	45
33	374	46
34	375	47
35	376	48
36	377	49
37	378	50
38	379	51
39	380	52
40	381	53
41	382	54
42	383	55
43	384	56
44	385	57
45	386	58
46	387	59
47	388	60
48	389	61
49	390	62
50	391	63

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
51	392	64
52	393	65
53	394	66
54	395	67
55	396	68
56	397	69
57	398	70
58	399	71
59	400	72
60	401	73
61	402	74
62	403	75
63	404	76
64	405	77
65	406	78
66	407	79
67	408	80
68	409	81
69	410	82
70	411	83
71	412	84
72	413	85
73	414	86
74	415	87
75	416	88
76	417	89
77	418	90
78	419	91
79	420	92
80	421	93
81	422	94
82	423	95
83	424	96
84	425	97
85	426	98
86	427	99
87	428	100
88	429	101
89	430	102
90	431	103
91	432	104
92	433	105
93	434	106
94	435	107
95	436	108
96	437	109
97	438	110
98	439	111
99	440	112
100	441	113
101	442	114
102	443	115
103	444	116

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
104	445	117
105	446	118
106	447	119
107	448	120
108	449	121
109	450	122
110	451	123
111	452	124
112	453	125
113	454	126
114	455	127
115	456	128
116	457	129
117	458	130
118	459	131
119	460	132
120	461	133
121	462	134
122	463	135
123	464	136
124	465	137
125	466	138
126	467	139
127	468	140
128	469	141
129	470	142
130	471	143
131	472	144
132	473	145
133	474	146
134	475	147
135	476	148
136	477	149
137	478	150
138	479	151
139	480	152
140	481	153
141	482	154
142	483	155
143	484	156
144	485	157
145	486	158
146	487	159
147	488	160
148	489	162
149	490	163
150	491	164
151	492	165
152	493	166
153	494	167
154	495	168
155	496	169
156	497	170

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
157	498	171
158	499	172
159	500	173
160	501	174
161	502	175
162	503	176
163	504	177
164	505	178
165	506	179
166	507	180
167	508	181
168	509	182
169	510	183
170	511	184
171	512	185
172	513	186
173	514	187
174	515	188
175	516	189
176	517	190
177	518	191
178	519	192
179	520	193
180	521	194
181	522	195
182	523	196
183	524	197
184	525	198
185	526	199
186	527	200
187	528	201
188	529	202
189	530	203
190	531	204
191	532	205
192	533	206
193	534	207
194	535	208
195	536	209
196	537	210
197	538	211
198	539	212
199	540	213
200	541	214
201	542	215
202	543	216
203	544	217
204	545	218
205	546	219
206	547	220
207	548	221
208	549	222
209	550	223

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
210	551	224
211	552	225
212	553	226
213	554	227
214	555	228
215	556	229
216	557	230
217	558	231
218	559	232
219	560	233
220	561	234
221	562	235
222	563	236
223	564	237
224	565	238
225	566	239
226	567	240
227	568	241
228	569	242
229	570	244
230	571	245
231	572	246
232	573	247
233	574	248
234	575	249
235	576	250
236	577	251
237	578	252
238	579	253
239	580	254
240	581	255
241	582	256
242	583	257
243	584	258
244	585	259
245	586	260
246	587	261
247	588	262
248	589	263
249	590	265
250	591	266
251	592	267
252	593	268
253	594	269
254	595	270
255	596	272
256	597	273
257	598	275
258	599	276
259	600	277
260	601	278
261	602	279
262	603	280

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
263	604	281
264	605	282
265	606	283
266	607	284
267	608	285
268	609	286
269	610	287
270	611	288
271	612	290
272	613	291
273	614	292
274	615	293
275	616	294
276	617	295
277	618	296
278	619	297
279	620	298
280	621	299
281	622	300
282	623	301
283	624	302
284	625	303
285	626	304
286	627	305
287	628	306
288	629	307
289	630	308
290	631	309
291	632	310
292	633	311
293	634	312
294	635	313
295	636	314
296	637	315
297	638	316
298	639	318
299	640	319
300	641	320
301	642	321
302	643	322
303	644	323
304	645	324
305	646	325
306	647	326
307	648	327
308	649	328
309	650	329
310	651	330
311	652	331
312	653	332
313	654	333
314	655	334
315	656	335

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/714,936
316	657	336
317	658	337
318	659	338
319	660	339
320	661	340
321	662	341
322	663	342
323	664	343
324	665	344
325	666	345
326	667	346
327	668	347
328	669	348
329	670	349
330	671	351
331	672	352
332	673	353
333	674	354
334	675	355
335	676	356
336	677	357
337	678	358
338	679	359
339	680	360
340	681	361
341	682	362

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-341, a mature protein coding portion of SEQ ID NO: 1-341, an active domain coding portion of SEQ ID NO: 1-341, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1;

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-341; and

(c) a polypeptide of any one of SEQ ID NO: 342-682.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from SEQ ID NO: 1-341, a mature protein coding portion of SEQ ID NO: 1-341, an active domain coding portion of SEQ ID NO: 1-341, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-341, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 342-682, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-341.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.